************ (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Jun 8 21:37:37 2000; MasPar time 14.11 Seconds 692.177 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-09-316-163-9 (1-207) _from US09316163.pep 1573 _ 1 EDCNELPPRRNTEILTGSWS......VEISCKSPDVINGSPISQKI/207

Scoring table: PAM 150

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum_Match 0% Lighting first 45 summaries

Database:

Statistics: Mean 41.851; Variance 66.119; scale 0.633 pir62 1:pjr1 2:pir2 3:pir3 4:pir4

pred. No. Ts the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222223	Result
1573 11573 1154 679 503 301 301 303 303 303 303 303 297 298 299 299 298 298 298 298 298 298 298	Score
100.0 73.4 43.2 32.2 21.2 21.2 21.2 21.2 21.2 21.2 2	Query Match
449 1231 1234 1659 1053 597 580 830 260 830 260 345 551 345 551 345 551 345 345 345 345	Query Match Length
	DB
NBHUHS NBHSH NBMSH S65551 S46199 S53711 T16833 JC5092 A30359 WMYVZSP A42755 I5383 NBMS A42755 I5382 NBMS A32606 A3	ID
complement factor H p complement factor H p complement factor H p factor H - bovine (fr probable complement r C4BP alpha chain prec hypothetical protein E-selectin - pig P-selectin precursor apolipoprotein H homo P-selectin precursor apolipoprotein H prec endothelial leukocyte endothelial leukocyte endothelial leukocyte apolipoprotein H prec decay-accelerating fa decay-accelerating fa endothelial leukocyte apolipoprotein H prec decay-accelerating fa	Description
0.00e+00 0.00e+00 0.00e+00 1.13e-265 5.85e-141 6.85e-146 6.02e-48 1.08e-47 1.08e-47 1.09e-46 1.69e-46 1.69e-46 1.69e-44 4.06e-44 4.06e-44 4.06e-44 4.06e-44 4.06e-44 5.22e-43 6.22e-43 6.22e-43	Pred. No.

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265	200	266	267	267	270	270	270	272	272	276	276	279	280	281	281	281	281	282	284	287
16.8	16.9	16.9		17.0	17.2	17.2	17.2	17.3	17.3	17.5	17.5	17.7	17.8	17.9	17.9	17.9	17.9	17.9	18.1	18.2
469	497	485	2489	2039	1091	610	345	369	362	1019	473	676	618	384	377	369	349	263	340	551
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NBMSC4	JC2054	S36772	173012	A28507	PL0009	I46001	NBHU	JC5138	JC5194	A38738	в38738	A45900	B42755	S01896	I54479	157998	G02913	C36838	156234	I46708
C4b-binding protein a	complement regulatory	E-selectin - bovine	complement C3b/C4b re	complement C3b/C4b re	complement C3d/Epstei	C4b-binding protein a	apolipoprotein H prec	membrane cofactor pro	membrane cofactor pro	coagulation factor C	coagulation factor C-	complement C3b recept	E-selectin precursor	membrane cofactor pro	membrane cofactor pro	membrane cofactor pro	sperm CD46 - human (f	complement control pr	decay-accelerating fa	endothelial leukocyte
.59e-	9.28e-38	w		5.42e-38	w	1.08e-38	1.08e-38	3.66e-39	3.66e-39	4.21e-40	4.21e-40	8.29e-41	4.82e-41	2.80e-41	2.80e-41	2.80e-41	2.80e-41	1.63e-41	5.49e-42	1.07e-42

partial contain #cross-references MUID: #accession A27877 ##molecule_type mRNA ##residues an a ##note Gl	REFERENCE #authors #journal #title	#cross-referent #accession ##status ##status ##mote ##residues	##DOCE ##DOCE REFERENCE #authors #journal #title	#cross-references MUID: #accession S03013 ##molecule_type mRNA ##residues 1-44 ##cross-references E	ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE DATE ACCESSIONS REFERENCE #authors #journal #title
cDNA sequence of the 38-kDa tryptic fragming the binding site for C3b. 87054207 870547 870547 870547 870547 870	AZ7877 Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P. Eur. J. Immunol. (1986) 16:1351-1355 Human complement factor H: isolation of cDNA clones and	ty_ty_e	matture protein was confirmed by protein sequencing 402-Tyr was also found A02-Tyr was also found A0238 Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802 Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts.	#cross-references MUID:88134059 #accession S03013 #accession S03013 ##molecule_type mRNA ##residues 1-449 ##label RIP ##residues 1-449 ##label RIP ##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492; ##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492;	NBHUHS #type complete complement factor H precursor, short splice form - human complement factor H-related protein: complement protein H #formal_ngme Homo sapiens #common_name man related protein H = 27-70n=193 #sequence_revision 23-Feb-1996 #text_change \$31-Dec-1993 #sequence_revision 23-Feb-1996 #text_change \$303013; B60238; A27877; A61103; A26505; S10479 \$00254 #text_change \$303013; B60238; A27877; Harris, T.J.R; Sim, R.B. Ripoche, J. (1988) 249:593-602 #text_change \$300015 #text_change \$300005 #text_change \$300005 #text_change \$300005 #text_change \$300005 #text_change \$300005 #text_change \$300005 #text_chan

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CLASSIFICATION
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              21 - 80
                                                       19-449
                                                                                                                                                                                                                                                                                                                                                      #map_position 1q32-1q32

the correspondence between the two loci and the sequences

indicated is unclear; factor H has been reported to have

several allelic forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references GDB:120041; OMIM:134370
#map_position 1q32-1q32
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#journal J. Immunol. (1986) 136:3407-3411

Structural analysis of human complement protein H: homology

#title with C4b binding protein, beta(2)-glycoprotein I, and the

Ba fragment of B.

#cross-references MUID:86169701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;
Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.
#journal Biochemistry (1992) 31:3626-3634
#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
#cross-references MUID:92232649
                                                                                                                                                                                                                     #pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 226-401,'Y',403-449 ##label KRI
##cross-references GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473
Tactor H has also been found bound to cell membranes in an unknown manner. However, it has at least one cell attachment site motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##status
##molecule_type mRNA
27-76 ##label SC2
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver. See also PIR:NBHUH.
                                                                                                                                                                                                       a cofactor in the inactivation of C3b by serine proteinase I; also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
                                                                                                                                     alternative splicing; complement alternate pathway;
                                                                                                                                                                                   #superfamily complement factor H; complement factor H repeat
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Sim, R.B.; DiScipio, R.G.
Biochem. J. (1982) 205:285-293
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Eur. J. Immunol. (1987) 17:1485-1489
Human complement factor H: expression of an additional truncated gene product of 43 kDa in human liver.
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                                                                                                                       glycoprotein; plasma
                        #domain signal sequence #status predicted #label SIG\
#product complement factor H, short splice form #status
experimental #label MAT\
       #domain
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complement factor H repeat homology #label FH01\
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#cross-references MUID:91184292
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178-205,210-251,
237-262,267-309,
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##cross-references EMBL:Y00716; NID:g31964; PIDN:CAA68704.1; PID:g31965
##note 402-Tyr was also found
##note parts of this sequence, including the amino and carboxyl
##note ends of the mature protein, were confirmed by protein
                                                                                                                                                                                                                          ##molecule_type mRNA
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Day, A.J.; Ripoche, J.; Lyons, A.; McIntosh, B.; Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived
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                                                                                                                                                                                                                                                                                                                                    A60238
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                                                                                                          only portions of this 4.3 kilobase mRNA were sequenced
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#title Sequence analysis of a cDNA clone encoding the C-terminal end
#cross-references MUID:88025472
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#title Partial characterization of human complement factor H by
protein and cDNA sequencing: homology with other complement
and non-complement proteins.
#cross-references_MUID:86188123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       module in solution.
#cross-references MUID:91278097
#contents annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;
pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.
#journal Biochemistry (1992) 31:3626-3634
#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
#cross-references MUID:92232649
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                                                                  #cross-references MUID:96205365
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#trosidues 'DFRN',579-1231 ##label DAY
##coss-references GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
##anote parts of this sequence were determined by protein
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##molecule_type protein
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Three-dimensional structure of a complement control protein
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                                                                                                                    A.; Gordon, D.L.; Burns, G.F.
Biochim. Biophys. Acta (1996) 1289:305-311
Factor H co-purifies with thrombospondin isolated from
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Cloning of the 1.4-kb mRNA species of human complement factor
H reveals a novel member of the short consensus repeat
family related to the carboxy terminal of the classical
                                                                                                                                                                                            Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano
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959-984,989-1032

357-385,389-431,

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##cross-references GDB:120041; OMIM:134370 #map_position 1q32-1q32 GENETICS
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver. See also PIR:NBHUHS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a cofactor in the inactivation of C3b by serine proteinase also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
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                                          #accession
                                                                                                                                                                                                                                                                                                     #authors Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y.
#journal J. Immunol. (1990) 144:358-362
#title Demonstration of an unusual allelic variation of mouse factor
#toross-references MUID:90111033
#cross-references MUID:90111033
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911
##molecule_type mRNA
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##residues 1-18 ##label RES
##cross-references GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729
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                                                                                         Biochemistry (1989) 28:9891-9897
Analysis of complement factor H mRNA expression:
Dexamethasone and IFN-gamma increase the level
                                            I49728
                                                                                                                                                    Munoz-Canoves, P.; Tack, B.F.; Vik, D.P.
                                                                                                                                                                                                                                                                                        I49711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kristensen, T.; Tack, B.F.

Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967

Murine protein H is comprised of 20 repeating units,

acids in length.
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Pred. No. 0.00e+00;
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597-622,629-672,

658-683,690-732,

718-743,752-791,

780-861,867-920,

836-861,867-920,

906-931,936-978,
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178-205,210-251,
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237-262,325-374,
357-385,389-431,
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                                                                              Match 73.4%;
Local Similarity 68.0%;
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##cross references GB.J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926
NT Two codominant alleles of factor H are present in mice.
NT Factor H functions as a cofactor in the inactivation of C3b by
serine proteinase I and also increases the rate of dissociation
of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5
| EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR
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                                                                                                                     #molecular-weight 139081 #checksum 3676
                                                            Score 1154; DB 1;
Pred. No. 1.13e-265;
33; Mismatches 33;
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                   #journal
#title
                                                      #authors
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                                                                                                                                                                                                                                                                                                                127 GQAVLPK 133
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                                                                                                                                                                                                                                                                                                                                                                                    FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                                                                                                                                                                                                                                                                         LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                             GSPISQK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soames, C.J.; Day, A.J.; Sim, R.B.
Blochem. J. (1996) 315:523-531
Prediction from sequence comparisons of residues of factor H
involved in the interaction with complement component C3b.
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19_Mar-1997_#sequence_revision 25-Apr-1997 #text_change
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factor H - bovine (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #length 669
Dahmen, A.; Kaidoh, T.; Zipfel, P.F.; Gigli, I.
Biochem. J. (1994) 301:391-397
Cloning and characterization of a cDNA representing a
putative complement-regulatory plasma protein from barred
                                                                                       13-Aug-1999
S46199; S77894
                                                                                                                                                                                 probable complement regulatory plasma protein SB1 - barred
                                                                                                                            #formal_name Parablax neblifer #common_name barred sand bass
19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change
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                                                                                                                                                                   sand bass
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Pred. No. 5.85e-141;
21; Mismatches 22;
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FHR3/
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#cross-references MUID:94318039
#accession $46199
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112-169
174-234
239-294
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                                                                                          50-107
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##residues 526-532,'x',534-537;809-817,'x',819-826 ##label DAH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 ABGNDFVFGSKVVYICQKGYQMVSRINYRRCVAEGWDGVVFVCESQQC-PLIHVDNNVQV 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 32.0%;
Local Similarity 41.8%;
                                                                                                                                                                                                                                                      ##residues
                                                                                                                                                                                    ##CTOSS-references EMBL: 235490 FICATION #superfamily C4b-binding protein alpha chain; complement
                                                                                                                                                                                                                                                                          ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                         de Frutos, P.G.; Dahlbaeck, B.
Blochim. Blophys. Acta (1995) 1261:285-289
Blochim. Blophys. Acta (1995) cDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein modules which bind C4b.
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#domain complement factor H repeat homology #label
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Pred. No. 6.86e-96;
29; Mismatches 68
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7 #checksum 8482
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#introns 14
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                                                                                                                                          170
                                                                                                                                                                225 VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNG 256
                                                                                                                                                                                               111 CDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD
                                                                                                                                                                                                                                  171 CSSNGEWTNEPANCKATECSRPSSPLHGKVVGSSL-T---YQ-S-VVTYSCDHGYRLVGQ 224
                                                                                                                                                                                                                                                                                                               117 AQWFGPD-LR-CKARACPDPGDIENG---LREGDTFEYPHHVKYSCNPGFLLVGSTS-RQ 170
                                                                                                                                                                                                                                                                            51 GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##experimental_source strain Bristol N2; clone T07H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##Cross-references EMBL:U53344; NID:g1255886; PID:g1255889
PIDN:AAA96225.1; GSPDB:GN00028; CESP:T0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **sudtus preliminary; translated from GB/EMBL/DDBJ ##molecule_type DNA ##mosessance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                                                                                                     Match 19.7%;
Local Similarity 33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 ISCKSPDVINGSPIS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 IINGK-HNGGNE-DIH-TYGSSVTYSCNPRFSLLGEASISCTVKNKTVGVWSPSPPVCKE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 VEVKT-D-FSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVEWSDPLPKCEIVKCEPPPN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 IICSPPNVPHGKIIS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 SDQTYPEGTQAIYKCRPGYRSLG-NVIMVCR-KGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 SENEYQTGTILKYTCRPGYTRNGLNPILTCKPRGLW-SYDTF--CVKKRCRNPGDLPNGQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 21.2%; Local Similarity 34.4%;
                                                                                                                           EEMHCSDDGFWSKEKPKCVEISCKS-PDVING 200
#-selectin - pig
#formal_name Sus scrofa domestica #common_name domestic pig
                                   E-selectin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14/1; 75/1; 102/3; 128/1; 186/1; 272/2; 326/1; 361/1; 422/1; 475/1; 527/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1996
The sequence of C. elegans cosmid T07H6.
T16833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESP: T07H6.5
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hypothetical protein T07H6.5 - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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#domain complement factor H repeat homology #label FH6\
#domain complement factor H repeat homology #label FH7\
#domain complement factor H repeat homology #label FH8
#th 597 #molecular-weight 66130 #checksum 6473
                                                   #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                #molecular-weight 61619 #checksum 2418
                                                                                                                                                                                                                                                                                                                                                    Score 310; DB 2; Length 560;
Pred. No. 3.60e-48;
36; Mismatches 51; Indels 14; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 334; DB 1; Length 597; Pred. No. 6.02e-54; 37; Mismatches 72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESP: T07H6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 15;
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##Cross-references GDB:120018; OMIM:173610
#map_position 1q22-1q25
CLASSIFICATION #superfamily complement factor H repeat homology;
                                                                                                                                     GENETICS
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240-298
303-361
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                                                                                                                                  ##cross-references GB.M25322
##note parts of this sequence, including the amino end of the mature protein, were confirmed by protein sequencing
                                                                                                                                                                                                                 ##molecule_type mRNA
##residues 1-830 ##label JOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSSLEV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 NHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQPKNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 TGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 QTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 19.6%; Score 308; DB 2;
Local Similarity 28.9%; Pred. No. 1.08e-47;
hes 52; Conservative 38; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-482 ##label WIN
##cross-references GB:U37521; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                           Johnston, G.I.; Cook, R.G.; McEver, R.P. Cell (1989) 56:1033-1044
Cloning of GMP-140, a granule membrane protein of platelets and endothelium: sequence similarity to proteins involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A30359 #type complete
P-selectin precursor - human
CD62 antigen; granule membrane protein 140 #
#formal_name Homo sapiens #common_name man
18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change
                                                                                                          GDB: SELP; GRMP
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#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4
gth 482 #molecular-weight 52341 #checksum 7729
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716,723,741
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                                                                                                           #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 GHWSAPLPTCEAISCEPLESPVHGS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 GFWSKEKPKCVEISCKSPDV-INGS 201
                                                                                                                                                                                                                                                                           ##experimental_source strain WR
NCE A42501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                     ##molecule_type DNA
##residues 1-263 ##label GOE
                                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:X13166;
                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
##cross-references GB:M35027; NID:g335317; PIDN:AAA47997.1; PID:g335345
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#length 830 #mo
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apolipoprotein H homolog precursor - vaccinia virus
                                                                                                        Winslow, J.P.; Paoletti, E. Virology (1990) 179:517-563
Appendix to "The complete DNA sequence of vaccinia virus". B42504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.
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phosphoprotein; surface antigen; transmembrane protein
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#domain EGF homology #label EGF\
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#domain intracellular #status predicted #label CYT\
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Pred. No. 1.08e-47;
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206-261
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86-143
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20-263
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#journal virology (1990) 179:247-266
#title The complete DNA sequence of vaccinia virus
#cross-references MUID:91021027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 HPTISNG 214
                                                                                                                                                                                             ##residues 1-768 ##label WEL
##cross-references GB:M87861; NID:g200552; PID:g200553
##experimental_source endothelial cells
                                                                                                                                                                             ##note
                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                      ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WINDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 LDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ANANYNIGDTIEYLCLPGYRKOKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
##status
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Similarity 34.8%;
65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD62; granule membrane protein 140; PADGEM #formal_name Mus musculus #common_name house mouse 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-sep-1997
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J. Biol. Chem. (1992) 267:15176-15183
Cloning of the mouse endothelial selectins. Expression obth E- and P-selectin is inducible by tumor necrosis
                                                                                                                                                                                                                                                                                                              A42755
                                                                 Molecular cloning and analysis of in vivo expression of murine P-selectin.
                                                                                                           Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L. Blood (1992) 80:795-800
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P-selectin precursor - mouse
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#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4
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                                                                                                                                                                             sequence extracted from NCBI backbone (NCBIP:109467)
    nucleic acid sequence not shown
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Pred. No. 1.69e-46;
28; Mismatches 76
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#accession I53821
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                                                                                                                                                                                                                                                                                                                                                                       ##Status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 HPIAAFAYDSSCKFECOPGYRARGSNTLHCTGSGOWSEDLPTCEAIACEPPEIPIHGS 334
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##cross-references GB:M72332; NID:g193565; PID:g193566
##note sequence extracted from NCBI backbone (NCBIP:109900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                                   Auchampach, J.A.; Oliver, M.G.; Anderson, D.C.; Manning, A.M. Gene (1994) 145:251-255
Cloning, Sequence comparison and in vivo expression of the gene encoding rat P-selectin.
                                                                                           #length 768
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Rattus norvegicus #common_name Norway rat 29-May-1998 #sequence_revision 29-May-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                  #domain C-type lectin homology #label ICH\
#domain EGF homology #label EGF\
#domain complement factor H repeat homology #label
                                                                                                                                                                                                                                                                                                                                                     preliminary; translated from GB/EMBL/DDBJ
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#domain complement factor H repeat homology #label FH01\
#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH07\
#domain complement factor H repeat homology #label FH07\
#domain complement factor H repeat homology #label FH08\
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33.1%;
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                                                                                 #molecular-weight 83516 #checksum 4885
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  Score 303; DB 2; Le
Pred. No. 1.69e-46;
33; Mismatches 75;
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No. 1.69e-46;
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28; Mismatches 46; Indels
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                                           Length 768;
Indels 10;
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Gaps
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FEATURE
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CLASSIFICATION #S
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                                 23-66,51-79,84-124,
110-137,142-188,
174-200,205-248,
174-200,205-248,
234-260,264-315,
300-307,325-345 #
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205-260
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105,117,162,183,
193
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1-251,'R',253-345 ##label SEL
##cross-references GB:S70439; NID:g546780; PIDN:AAB30789.1; PID:g546781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##experimental_source liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 REYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 FECOPGYRMRGSDILHCTDSGOW-S-EPLPTCEAIAC-EPLESPLHGSMDCFPSTGAFGY 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 GPLKYQSACSFSCDEGSLLVGASVIRCLATGHWSEAPPECQAVSCTP 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GVKAVYTCNEGYQLLGEINYREC-DTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPD 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                               chylomicron; duplication; glycoprotein; HDL; heparin binding;
                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily apolipoprotein H; complement factor H repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sellar, G.C.; Steel, D.M.; Zafiropoulos, A.; Seery, L.T.; Whitehead, A.S.
Biochem. Biophys. Res. Commun. (1994) 200:1521-1528
Characterization, expression and evolution of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B2gp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics (1992) 13:1082-1087
Molecular cloning of mouse beta-2-glycoprotein I and mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #type complete
apollipoprotein H practursor - mouse
50K serum glycoprotein; activated protein C-binding protein;
beta-2-glycoprotein I
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                                                                                                                                                                                                                                                                                                                                                                                                          homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the gene to chromosome 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-May-1999
                                                                                                                                          #domain signal sequence #status predicted #label SIG\
#product apolipoprotein H *status predicted #label MAT\
#domain complement factor H repeat homology *label FH1\
#domain complement factor H repeat homology *label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH4\
                              #disulfide_bonds #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ala and ATG for residue 278 as Asn
sequence extracted from NCBI backbone (NCBIN:111791,
NCBIP:111794) and corrected to correspond with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the authors translated the codon ACT for residue 253 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-252, 'A', 254-277, 'N', 279-345 ##label NON
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#binding_site carbohydrate (Asn) (covalent) #status

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12-138
180-237
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Best Local
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Shows, T.; Gimbrone Jr., M.A.; Bevilacqua, M.P.

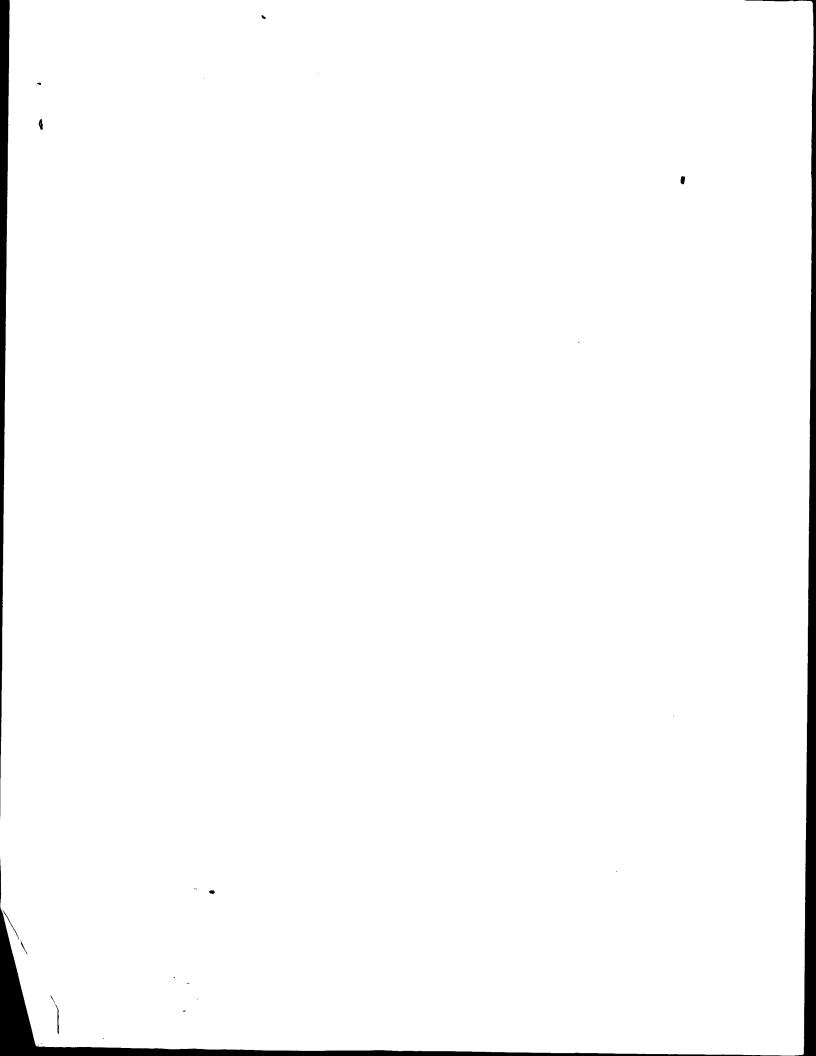
#journal J. Biol. Chem. (1991) 266:2466-2473

#title Structure and chromosomal location of the gene for endothelial-leukocyte adhesion molecule 1.

#cross-references.MUID:91115870
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367-425
430-488
493-547
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Local Similarity 29.08;
es 51; Conservation
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                                                                         210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
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   34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
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|llarity 27.4%;
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                                                                                                                                                      Pred.
33; 1
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Pred. No. 2.63e-45;
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Search completed: Thu Jun Job time: 17 secs.

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Best Local Similarity 27.4%;
Matches 45; Conservative
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367-425
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     HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endothelial leukocyte adhesion molecule precursor - human #formal_name Homo sapiens #common_name man 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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#domain complement factor H repeat homology #label FH08\
#domain complement factor H repeat homology #label FH09\
#domain complement factor H repeat homology #label FH10\
#domain complement factor H repeat homology #label FH11\
#domain complement factor H repeat homology #label FH12
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#product endothelial leukocyte adhesion molecule 1
#status predicted #label MAT\
#domain EGF homology #label EGF\
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Pred. No. 2.63e-45;
33; Mismatches 79;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Jun 8 21:38:42 2000; MasPar time 21.93 Seconds 654.600 Million cell updates/sec

Description: Perfect Score: >US-09-316-163-9 (1-207) from US09316163.pep 1573

Sequence: 1 EDCNELPPRRNTEILIGSWS.....VEISCKSPDVINGSPISQKI 207

Scoring table: PAM 150 Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_iffertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 41.889; Variance 59.758; scale 0.701

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query Match	Length	BIG	ID	Description	Pred. No.
ا د	1573	100.0	449	4.	Q14570	z	0
N	679	43.2	669	σ	Q28085	CCP MODULES 3-12, WITH	4.01e-1
ω	503	32.0	1053	13	Q91275	COMPLEMENT REGULATORY	3.14e-106
4	364	23.1	645	14	Q9WRU2	COMPLEMENT BINDING PRO	6.97e-68
5	344	21.9	550	14	040912	ORF 04.	1.73e-62
თ	343	21.8	550	14	P88903	ORF 4.	
7	320	20.3	360	14	Q9YTQ8	COMPLEMENT CONTROL PRO	4.56e-5
œ	316	20.1	259	14	P87616	41KBP FRAGMENT FROM LE	
9	312	19.8	754	σ	Q28290	CELL ADHESION MOLECULE	6.08e-54
10	310	19.7	560	ۍ	Q22328	COSMID T07H6.	2.06e-53
11	308	19.6	482	σ	Q28982	E-SELECTIN.	6.98e-53
12	304	19.3	657	4	Q14006	COMPLEMENT H FACTOR (F	7
13	297	18.9	740	4	095508	DJ780M13.1.2 (SELECTIN	ر. د
14	295	18.8	347	4	P78361	DECAY-ACCELERATION FAC	<u></u>
15	293	18.6	533	11	008569	ACROSOMAL MATRIX COMPO	6.29e-49
16	290	18.4	417	11	035520	512 ANTIGEN (FRAGMENT)	3.85e-48
17	290	18.4	559	11	Q63135	COMPLEMENT REGULATORY	· w
18	288	18.3	740	4	095507	DJ780M13.1.1 (SELECTIN	.
19	286	18.2	222	σ	019122	MEMBRANE COFACTOR PROT	4.
20	284	18.1	363	6	002839	PORCINE MEMBRANE COFAC	1.43e-45

4 5	44	43	42	41	40	39	38	37	36	3 5	34	3 3	32	3 <u>1</u>	30	29	28	27	26	25	24	23	22	21
266	266	266	266	267	267	269	269	270	270	270	272	274	275	279	279	278	278	280	280	282	281	282	282	282
16.9	16.9	16.9	16.9	17.0	17.0			17.2	17.2	17.2	17.3	17.4	17.5	17.7	17.7	17.7	17.7	17.8	17.8	17.9	17.9	17.9	17.9	17.9
497	336	314	222	2489	2039	1083	1019	1032	285	222	369	377	974	679	646	285	285	383	263	378				263
11	σ	σ	σ	4	4	ഗ	υ	4	σ	σ	σ	σ	u	11	σ	σ	σ	11	14	6	4	14	14	14
Q63612	062834	062835	019124	Q16744	Q16745	Q26423	Q26422	Q13866	019121	019128	P79138	062838	P91658	Q9925 4	Q29097	019127	019126	Q9WTI9	Q89076	062837	Q15429	Q89859	089061	Q07033
512 ANTIGEN PRECURSOR.	MEMBRANE COFACTOR PROT	COFACTOR		\sim	COMPLEMENT RECEPTOR 1.	FACTOR C.	FACTOR C.	CR2 RECEPTOR PRECURSOR	MEMBRANE COFACTOR PROT	MEMBRANE COFACTOR PROT				COMPLEMENT RECEPTOR TY	P-SELECTIN PRECURSOR.	MEMBRANE COFACTOR PROT	MEMBRANE COFACTOR PROT	DECAY - ACCELERATING FAC		MEMBRANE COFACTOR PROT	CD46.	HOMOLOG OF VACCINIA VI		D12L PROTEIN.
6.83e		6.836-			:	1.14e-42	٠	٠		6.30e-43	٠.		3.17e-44	•			5.26e-45	٠	1.59e-45			•		

, Q	FT SQ	DR DR	DR	다 다 다	DR 2	RA	RP	RN PL	RA 7	RN	RL.	꼽	RA	RX	מ מ צ	RL	RT	RΑ	RX '	d X	8	8	os:	N E	ğ	ΡŢ	Di.	3 5	RESULT
Query Match	Signal. SIGNAL CHAIN SEQUENCE	יי וזי		EMBL; M12.			UENCE	Submitted	VIK D.P.,		J. Immunol.	"Structural anal binding protein,	KRISTENSEN T.,		SECURIOR O	BiochemJ	"The compl	RIPOCHE J.	MEDLINE; 8		Eutheria;	Eukaryota;	Homo sapiens	HE OR CEH.	01-NOV-1999	01-NOV-1996	01-NOV-1996	•	LT 1
100.0%; Score 1573;	1 18 POTENTIAL. 19 449 POTENTIAL. 449 AA; 51033 MW; 61231E1B	P10998; IVVC. PF00084; sushi; 7.	CAA82763	M12383; AAA52U13.1; U56979; AAB01987.1;	CAA30403.1;	/1993) Trmunologia Hospital Trias	OF 1-9 FROM N.A.		WILLIAMS S.A.;	1-10	ol. 136:3407-3411(1986).	"Structural analysis of numan complement binding protein, beta 2-glycoprotein I,		169701.	OF 226-449 FROM N.A.	Biochem 249:593-602(1988).	"The complete amino acid sequence of human	?	88134059.	P NORTH	Primates; Catarrhini; Hominidae;	etazoa; Chordata; Cr	ens (Human).	I PACION D PRECONSON.	9 (TrEMBLrel. 12, Last	(TrEMBLrel. 01, Last	(TrEMBLrel. 01, Creat	435.	DESTIMINARY: DRT: 449
DB 4; Length 449;	CRC32;					as I Puiol, Spain.		/DDBJ databases.				and the Ba fragment of B2.	1				an complement factor H.";	.B.;			e; Homo.	н			annotation update)	update)		:	P

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Q91275;
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Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 12, Last annotation update)
Q1-NOV-1999 (TREMBLrel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
Paralabrax nebulifer (barred sand bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Theory of the control of the contr
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"Prediction from sequence comparisons of residues in the interaction with complement component C3b."
Biochem. J. 315:523-531(1996).
EMBL; X98697; CAA67257.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
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les 84; Conservation
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75683 MW; FAFOD174 CRC32;
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Pred. No. 4.01e-156;
21; Mismatches 22; Indels
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                                        Acanthopterygii; Percomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.1%; Score 364; DB 14; Best Local Similarity 32.6%; Pred. No. 6.97e-68; Matches 61; Conservative 40; Mismatches 71
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Best Local Similarity 41.8%;
Matches 76; Conservative
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SEARLES R.P., BERCOUAM E.P., AXTHELM M.K., WONG S.W.;

"Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8.";
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01-NOV-1999 (TREMBLrel. 12, Last sequence update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
COMPLEMENT BINDING PROTEIN.
Macaca mulatta rhadinovirus 17577.
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
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Virol. 73:3040-3053(1999).

TOTAL NAME OF THE PROPERTY OF T
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                                                                                                                                        455 ITNGKY--HPVK-DF-YQYLDTVTFSCNRDFSLVGDEMTTCISNT-WNKPFPRCEQITCS 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9WRU2;
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                                                                                                                                                                                                                                                                                                           395 VTSGEDAFKYGTNITYKCNEGYQLLGSMYRICMLKDDLKTVDWEPKAPICDIEKCKPPPQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 EKYSVGASVELICRPGFTKMQSTVSVECLSNGTWTAPNA--KCHRKKCPTPQELLNGEYI 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94318039.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                      22 QTYPEGTQAIYKCRPGYRSLGNVINV-C-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
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                                                      PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                         LTGG-NVFEYGVKAVYTCNEGYQLLGE-IN-Y--REC-DTDGWTNDIPICEVVKCLPVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF083501; AAD21332.1; -.
NCE 645 AA; 71526 MW; 60FB82D6 CRC32;
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Pred. No. 3.14e-106;
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                                                  MOORE P.S., BASHOFF C., WEISS "MOLECULAR minicry of human ogenes by KSHV."; Science 274:1739-1744(1996). EMBL; U75698; AAC57082.1; -. HSSP; P10998; IVVC.
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040912;
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"Cell-homologous genes in the Kaposi's sarcoma-associated human herpesvirus 8: determinants of its pathogenicity?";

J. virol. 71:4187-4192(1997).

EMBL; U93872; AAB62602.1;

HSSP; P10998; 1VVC.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
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SEQUENCE 550 AA; 60648 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
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                                                                                                                                                                                                                                                                                                                                                 RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97094384.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
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     SEQUENCE
                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             ( BAHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \frac{3}{3}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 RCRSGYTTYARNITATCLQGGTW-S-EPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
                                 PF00084;
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                                                                                                             274:1739-1744(1996).
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(TrEMBLrel. 12, Last annotation update)
        550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.9%;
larity 33.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
     A
A
                                 sushi; 4
     60687 MW;
                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                         WEISS R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 344; DB 14;
Pred. No. 1.73e-62;
38; Mismatches 64
                                                                                                                                                                cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                    93:14862-14867(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558089B4 CRC32;
     CEA2CAEC CRC32;
                                                                                                                                                                                         CHANG Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 550;
                                                                                                                                                             cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels 17;
                                                                                                                                                                   response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.3%;
Best Local Similarity 37.6%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                      P87616;
P87616;
01-MAY-1997
01-MAY-1997
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9YTQB;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALBRECHT J.-C., FLECKENSTEIN B.;
"Primary Structure of the Herpesvirus Ateles Genome.";
submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF083424; AAC95530.1;
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ateline herpesvirus 3. Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gammaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8OTY60
SEQUENCE FROM N.A. STRAIN-GRI-90;
                                                                                                                                             Cowpox virus (CPV).
                                                                                                                                                                    D17L OR C17L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
                                                                                     Orthopoxvirus.
                                                                                                            Viruses; dsDNA viruses,
                                                                                                                                                                                                  41KBP FRAGMENT FROM LEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 CKSPDVING 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 21.8%;
Local Similarity 33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 CKIPQVANG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 ANGT--HTNIK-E-YYTYLDAVTYSCNDETKLTLTGPSSKQCSETGRWVPDEETKCEFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 VTG-NLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRVNWTPRPPICEITKCKPPPTI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-H-R-P---KIKNGDF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTGGNVFEYGVKAVYTCNEGYQLLGEINYREC -- DTDG -- - WTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFT
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                                                                                                                                                                                                                         (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40208 MW; F66C7ADA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhadinovirus
                                                                                                                                                                                               03, Created)
03, Last sequence update)
12, Last annotation update)
T END OF GENOME.
                                                                                                               no
                                                                                                               RNA stage;
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Pred. No. 3.22e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.56e-56; 28; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Mismatches
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                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                  Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14;
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                                                                                                                  Chordopoxvirinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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Best Local S
Matches 7
   Query Match
                                 SEQUENCE
                                                 CHAIN
                                                                                                                                                      MANNING A.M., SANDERS W.E. JR., KUKIELKA G.L., DORE M., ROSENBLOOM C.L., HAWKINS H.L., MICHAEL L.H., ENTMAN M.L BEAUDET A.L., ANDERSON D.C.; Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases EMBL; M88170; AAA63789.1; -.
HSSP; P16109; 1FSB.
                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; 1
PRAM; PF00059; lectin_c; 1.
PFAM; PF00084; sushi; 8.
Signal; Cell adhesion; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TremBlrel 01, 01-NOV-1996 (TremBlrel 01, 01-NOV-1999 (TremBlrel 12,
                                                                                                                                                                                                                                                TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                NON_TER
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Eutheria; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                            GMP140
                                                                                                                                                                                                                                                                                                                                                     CELL ADHESION MOLECULE PRECURSOR (FRAGMENT).
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Virology 243:432-460(1998).
EMBL; X94355; CAA64102.1; -.
EMBL; Y11842; CAA72567.1; -.
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHCHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A., RYAZANKINA O.I., GUTOROV V.V., KOTWAL G.J.; "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97068532.

SAFRONOV P.F., PETROV N.A., RIAZANKINA O.I., TOTMENIN A.V., SHCHELKUNOV S.N., SANDAKHCHIEV L.S.;

"Genes of a circle of hosts for the cowpox virus.";

"Genes of a circle of hosts for the cowpox virus.";

Dokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 DGFWSKEKPKCVEISCKSPDVING 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 CCPIPSRPITMKFKGT-VDSHYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.1%;
Local Similarity 34.8%;
es 71; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPEAPICESVKCQSPPSISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCIKRRCPSPRDIDNGQLDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00084;
                                754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sushi; 4.
                                                                                                                                   C_TYPE_LECTIN_1; 1.
 19.8%;
                                82303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28193 MW;
 Score 312;
                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 316; DB 14;
Pred. No. 5.28e-55;
30; Mismatches 84
                                            POTENTIAL.
CELL ADHESION MOLECULE.
                            E9570281 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76531F63 CRC32;
                                                                                                                                                                                                                                                                                            Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 84; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                               754 AA.
DB 6;
Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 259;
                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                               SMITH C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ULT 10
Q22328
Q22328;
Q22328;
Q1-NOV-1996 (Tremblrel 0
01-NOV-1996 (Tremblrel 0
01-NOV-1996 (Tremblrel 1
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U53344; AAA,96225.1; -. HSSP; P10998; 1VC. PFAM; PF00084; sushi; 7. SEQUENCE 560 AA; 61619 MW; 3A10AF63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONFIELD J., BURTON J., CONNELL M., COPSEY T., COODER J., COULSON CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRRILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M. PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEL SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATERSTON R., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94150718.
WILSON R., AINSCOUGH R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
225 VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COSMID T07H6.
                                                              111 CDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD
                                                                                                                  171 CSSNGEWINEPANCKATECSRPSSPLHGKVVGSSL-T---YQ-S-VVIYSCDHGYRLVGQ 224
                                                                                                                                                                                                                                     117 AQWFGPD-LR-CKARACPDPGDIENG---LREGDTFEYPHHVKYSCNPGFLLVGSTS-RQ 170
                                                                                                                                                                                 51 GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 PDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 SFY-CTEGYELNGPSKLECLASGTWIN-KPPR-CVATQC-PPLKTPEQGSMNCLHSVEAF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSRAFQYNTSCRFHCAEGFRLEGADLVQCTDLGQWTAPAPACQALQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAME
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                                                                                                                                                                                                                                                                                                    19.7%;
Similarity 33.6%;
51; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APR-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oda; Secernentea;
Rhabditidae; Pelc
                                                                                                                                                                                                                                                                                                       Score 310; DB 5; Le
Pred. No. 2.06e-53;
36; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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oderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                            Length 560;
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                                                                                                                                                                                                                                                                                                    Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D., SHOWNKEEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COULSON A.,
                                                                                                                                                                                                                                                                                                    Gaps
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Best Local :
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Best Local
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                                                                                                                                                                                                               O14006 PRELIADATE O14006 PRELIADATE O14006; Q14006; Q14006; Q14006 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-NOV-1999 (TrEMBLrel. 12, Last annotation update) O1-NOV-1999 (TREMBLREL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00008; EGF; 1.
PFAM; PF000059; lectin_c; 1.
PFAM; PF00084; sushi; 4.
PRINTS; PR00043; SELECTIN.
Lectin; Glycoprotein.
SEQUENCE 482 AA; 52341 MW;
                                       NON_TER
SEQUENCE
                                                                            MEDIINE; 88025472.

DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B., "Sequence analysis of a CDNA clone encoding thuman complement factor H."; blosci. Rep. 7:201-207(1987).

EMBL, M1517; AAA52016.1; -.

HSSP; P08603; 1HFH.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                    PFAM;
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                   Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U37521; AAC48680.1; -.
HSSP; P16581; 1ESL.
PROSITE; PS00615; C_TYPE_LECTIN_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The intron-exon structure of Gene 176:67-72(1996).
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                                                                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                                                                                                                                                                             313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSSLEV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                           254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           81 TGGNVFEYGVKAV - - YSCNEGYQLLGEINYRECDIDG-WINDIPICEVVKCLPVTAPENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                                                                                                                                                                                                                                                                      KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NHSSIGEFAYKSTCHFTCAEGFGLOGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQPKNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                 PF00084; sushi; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97075911
                                         657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                        AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%;
28.9%;
19.3%;
27.1%;
                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
Score 304; DB 4;
Pred. No. 7.96e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 308; DB 6;
Pred. No. 6.98e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.98e-
38; Mismatches
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                                       F4AB5238 CRC32;
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                                                                                                                                 the
                                                                                                                                            HARRIS T.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 482;
           Length
                                                                                                                                 C-terminal
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                                                                                                                                end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                       P78361 PRELIMINARY; PRT; 347 AA.
P78361,
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DECAY-ACCELERATION FACTOR (FRAGMENT).
                    TISSUE-BRAIN HIPPOCAMPUS;
KUMAR V.B., HYUNG C., NAK
                                                                                  Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O95508 PRELIMINARY; PRT; 740 AA.
095508; 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLREL) 12, Last annotation update)
01-NOV-1999 (TrEMBLREL) 12, Last annotation update)
       Submitted
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
NON_TER 740 740
SEQUENCE 740 AA; 81390 MW; 5CEFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL022146; CAA18143.1;
HSSP; P16109; 1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD62, GMP140)) (ISOFORM 2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                   139
                                                                                                                                                                                                                                                                                                                                            397 -VNCS-HPFGAFRY-QSVCSFTCNEGLLLVGASVLQCLATGNWNSVPPECQAIPCTP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 AFAYGSSCKFECQPGYRVRGLDMLRCIDSGHWSA--PLPTCEAISC-EPLESPVHGSMDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IOWDEN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 KEKPKCVEISC-KSPDVINGSPISOKI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 CEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKCFEGFGIDGPAIAK-CLGEKWSHP-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 CSQ-PPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKW-S-SP-PQ 351
                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 TYPEGTQAIYKCRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPF-GTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CNELPPRRNTEILTGSWSDQ-TYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK 61
                                                                                                                                                                                                                                                                                                                                                                                  TGG-NVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                             IVSSAMEPDREYHFGQAV-RFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS
                                                                                                                                                                                                                                                                                                                                                                                                                    SPSLRAFQYDTNCSFRCAEGFMLRGADIVR-CDNLGQWTAPAPVCQALQCQDLPVPNEAR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GRPTCRDTSCVNPPTVQNAYIVSRQM 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQVTYTCATYYKMDGASNVTCINSR-WT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
., HYUNG C., NAKRA R., WALTERS M., SA (FEB-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.9%; ilarity 28.8%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 297; DB 4; Length 740; Pred. No. 5.58e-50; 39; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5CEFCCF0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                   SASSER T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
   databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                    BERNARDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSTER J.A., FRIDAY B.B., MAULIT M.T., BLOBEL C., WINFREY V.P., OLSON G.E., KIM K.S., GERTON G.L.;
"AM67, a secretory component of the guinea pig sperm acrosomal matrix, is related to mouse sperm protein sp56 and the complement component 4-binding proteins.";
J. Biol. Chem. 272:12714-12722(1997).
EMBL; 075654; AAC13888.1; -.
HSSP; P10998; 1VVC.
PPFAM; PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O08569; PRELIMINARY; PRT; 533 AA.

O08569; O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)
O1-JUL-1999 (TrEMBLrel. 12, Last annotation update)
ACROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U88576; AAB48622.1;
HSSP; P08603; 1HCC.
PFAM; PF00084; sushi; 4.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-HARTLEY; TI MEDLINE; 97284752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 1
SEQUENCE 347 AA; 37847 MW; 23A2A260 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 VNNDEGEWSGPPPEC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 234
218 CRQPHIPKG 226
                                                                136 NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHC--SDD--GFWSKEKPKCVEIS 191
                                                                                                                                                                                                                                                                       104 IIT-DLL-FGSTIEFSCSKGYSLIGSTT-SQCESQGKTVDWSDPLPECVIVKCDSPPDIS 160
                                                                                                                                 161 NGK-HSGT-DEDL-YTYGSLVTYVCDPNYSLLGNASISCLVANKTVGVWSSNPPTCEKVI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 18.6%; Score 293; DB 11; Length 533; Local Similarity 27.0%; Pred. No. 6.29e-49; hes 51; Conservative 51; Mismatches 69; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 18.8%;
Local Similarity 29.7%;
es 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                         80 LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTAPE 135
                                                                                                                                                                                                                                                                                                                                           21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
                                                                                                                                                                                                                                                                                                                                                                                   ETNERTGTALKYNCHRGYWRVNSSHVICDINGSWI-YNVF--CAKKRCRNPGELANGKVE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATITFSCNTGYKLFGSTSSFCLISGSSVQ 178
                                                                                                                                                                                                                                                                                                                                           DQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 28 F
29 533 A
533 AA; 59772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 295; DB 4; Length 347; pred. No. 1.87e-49; 43; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

ACROSOMAL MATRIX COMPONENT AM67.

; 60EEA526 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps 12;
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QY 192 CKSPDVING 200

Search completed: Thu Jun 8 21:39:08 2000 Job time: 26 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:38:12 2000; MasPar time 8.92 Seconds 706.532 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-316-163-9 (1-207) from US09316163.pep 1573

Sequence: 1 EDCNELPPRRNTEILTGSWS......VEISCKSPDVINGSPISQKI 207

Scoring table:

PAM 150 Gap 11

83857 secs, 30454973 residues

Database:

Post-processing: Minimum Match 04 Listing first 45 summaries

swiss-prot38

Statistics: Mean 42.607; Variance 59.776; scale 0.713

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 4 4 4 4 6 5 7 7 7 10 11 11 11 11 11 11 11 11 11 11 11 11	Result
11573 3084 3088 3083 3083 3033 3033 3033 303	Score
100.0 73.4 19.6 19.6 19.3 19.3 19.3 19.3 18.9 18.9 18.9 18.3 18.3 18.3 18.3 17.3 17.3	Query Match 1
1231 484 483 830 263 768 345 345 345 345 345 345 345 345 345 345	Length
	DB E
CFAH_MOUSE LEM2_PIG LEM3_HUWAN VCP_VACCV LEM3_MOUSE LEM3_MOUSE LEM3_HOWAN APOH_BOVIN DAF_HUWAN CABP_HUWAN CABP_HUWAN CCPH_HSVSA LEM2_RABIT LEM2_RABIT LEM2_RABIT LEM2_RABIT LEM2_RABIT LEM2_RABIT LEM2_CAVPO LEM3_CAVPO LEM4_CAVPO LEM4_CAVPO LEM4_CAVPO LEM4_CAVPO LEM4_CAVPO LEM5_CAVPO LEM5	ID
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SEQUENCE OF 19:35: MEDLINE; 83048213. Sim R.B., Discipio R.G.; Purification and structural studies on the complement-system control protein beta 1H (Factor H).";	UENCE OF 1047- LINE; 91201892 aller C., Kois oning of the 1 eals a novel m the_carboxy.te Immunol. 146:3	Immunol OF 226 861697 en T., en Tal ana protein ol. 136	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=LIVER; MEDLINE; 88134059. Ripoche J. Day A.J., Harris T.J.R., Sim R.B.; "The complete amino acid sequence of human complement factor H."; Biochem. J. 249:593-602(1988). [2] SEQUENCE OF 53-445 FROM N.A. MEDLINE; 87054207. SChulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; SCHULZ T.F., Schwaeble W., Stanley K.K., Weiss and partial cDNA "Human complement factor H: isolation of cDNA clones and partial cDNA sequence of the 38-kDa tryptic fragment containing the binding site	CFAH_HUMAN STANDARD; PRT; 1231 AA. CFAH_HUMAN STANDARD; PRT; 1231 AA. P08603; P01-AUG-1988 (Rel. 08, Created) O1-AUG-1990 (Rel. 39, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) COMPLEMENT FACTOR H PRECURSOR. HF1 OR HF OR CFH. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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EMBL; Y00716; CAA68704.1; -...
EMBL; X04697; CAB41739.1; ALT_FRAME.
EMBL; M65294; AAA35948.1; -...
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J. Mol. Biol. 232:268-284(1993).

-i. FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEXENT PATHWAY.

-i. SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.

-i. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J.,

Driscoll P.C., Sim B., Campbell I.D.;
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Biochemistry 31:3626-3634(1992).
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MEDLINE; 92232649.
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Norman D.G., Barlow P.N., Baron M., Day A.J., Sim B., Campbell I.D., "Three-dimensional structure of a complement control protein module in solution.";

1. Mol. Biol. 219:717-725/1001.
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01-JAN-1988 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1-H).
                                                                                                                                                                                                                                                                   Munoz-Canoves P., Tack B.F., Vik D.P.;
"Analysis of complement factor H mRNA expression: dexamethasone IFN-gamma increase the level of H in L cells.";
Biochemistry 28:9891-9897(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Eutheria; Rodentia;
                           culties requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                      "Demonstration of an unusual allelic variation of mouse factor H by the complete cDNA sequence of the H.2 allotype.";

Inmunol. 144:358-362(1990).

-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BB COMPLEX (C3 CONVERTASE) AND THE (C3B)NB COMPLEX (C5 CONVERTASE) AND THE (C3B)NB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

-i- POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
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EMBL; M12660; AAA37759.1; -. EMBL; J02891; AAA37795.1; -. EMBL; M31979; AAA37762.1; -.
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                                                        SWISS-PROT entry is copyright. It is produced through a collaboration reen the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by another the statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial
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Matches 14
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European, Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 201:805-805(1994).

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED B. ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES (ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES (ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES (ELAM-1 IS SIALYL-LEWIS X (ELAM-1 IS SIALYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsang Y.T.M., Haskard D.O., Robinson M.K.; "Cloning and expression kinetics of porcine vascular cell adhesion molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-AORTIC ENDOMEDLINE; 94271236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-AORTIC ENDOTHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEM2_PIG
P98110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular and functional analysis of potential role in xenograft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rollins S.A., Evans M.J., Johnson K.K., Elliot E.A., Matis L.A., Rother R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSUE-AORTIC
                                                                                                                                                                           FUNCTION: PLAYS AN IMPORTANT ROLE IN ACUTE CELLULAR ALLOGRAFT REJECTION AND PROBABLY ALSO IN XENOGRAFT REJECTION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 4 SUSHII (SCR) REPEATS; PORCINE E-LECTIN LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                               THE HUMAN SUSHI-1 AND -4 EQUIVALENTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDCKGPPPRENSEILSGSWSEQLYPEGTQATYKCRPGYRTLGTIVKVCKNGKWVASNPSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biophys.
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Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1030
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Conservative
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Pred. No. 6.87e-299;
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DISULFID
                                                                                                196 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                                                                                                                                                                                                                CONFLICT
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DOMAIN
                              254 NHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQPKNG
                                                                                                                                                                                                                                                                                                                                  CONFLICT
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PEAM; PF00059; lectin_c; 1.
PEAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00343; SELECTIN.
PROSITE; PS00122; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selectin; Signal;
81 TGGNVFEYGVKAV-~YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG
                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L39076; AAA61545.1; -. EMBL; U08350; AAA21541.1; -. HSSP; P16581; 1ESL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified
                                                                QTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adhesion; Transmembrane;
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long as its content and this statement is not removed. Usage by ar
                                                                                                                                                                                                             484 AA;
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                         19.6%;
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                                                                                                                                                                                                                                              52567 MW;
                                                                                                                                   Score 308; DB 1;
Pred. No. 8.32e-54;
38; Mismatches 82
                                                                                                                                                                                                                                                       POTENTIAL.

POTENTIAL.

C -> Y (IN REF. 2).

L -> F (IN REF. 2).

T -> N (IN REF. 2).

K -> N (IN REF. 2).

V -> A (IN REF. 2).

V -> M (IN REF. 2).
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RESULT TO SOLUTION OF THE SOLUTION O
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Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
Ra Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
The P-selectin gene is highly polymorphic: reduced frequency of the prof15 allele carriers in patients with myocardial infarction.";
Lum. Mol. Genet. 7:1277-1284(1998).
Lum. Mol. Genet. 7:1277-1284(1998).
C. -i- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
C. -i- FUNCTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
C. INTERRACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS
C. INTERRACTION: TYPE I MEMBRANE PROTEIN
C. -i- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANDLES OF PLATELETS
C. AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
C. MINISTER CONTROL OF CONTROL OF CONTROL OF CELL
C. MINISTER CONTROL OF 
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P16109;
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Ol-APR-1990 (Rel. 15, Last sequence update)
Ol-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
P-SCAC (FRIKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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Johnston G.MP-140, a granule membrane protein of platelets and "Cloning of GMP-140, a granule membrane protein of platelets and endothelium: sequence similarity to proteins involved in cell adhesion and inflammation.";
Cell 56:1033-1044(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bajorath J., Stenkamp R., Aruffo A.;

"Knowledge-based model building of proteins: concepts and examples.";

Protein Sci. 2:1798-1810(1993).
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                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
EMBL; M60234; AAA35910.1; EMBL; M60217; AAA35910.1;
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 9 SUGHI (SCR) REPEATS.
SIMILARITY: CONTAINS 9 SUGHI (SCR) REPEATS.
DATABASE: NAME-PROW: NOTE-CD guide CD62P entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
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PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
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Best Local
                                                                                                                     Motival G.J., Moss B.;

Kotwal G.J., Moss B.;

"Analysis of a large cluster of nonessential genes deleted

vaccinia virus terminal transposition mutant.";

Virology 167:524-537(1988).
                                             MEDLINE;
                                                             STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                           Kotwal G.J., Moss B.;
"Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     STRAIN-WR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 OCLAAOC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 55; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHWSAPLPTCEAISCEPLESPVHGS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFWSKEKPKCVEISCKSPDV-INGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
     S.J., /Johnson G.P., Perkus M.E., Davis
                                          91021027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                88318974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.6%;
26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 308; DB 1;
Pred. No. 8.32e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T -> P (REDUCED FREQUENCY IN PATIENTS WITH MYOCARDIAL INFARCTION).
/FTId=VAR_004195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENDOCYTOSIS SIGNAL (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTId=VAR_004192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FBC407BA2579F6EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ā
S.W., Winslow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 830;
                                                                                                                                                                          from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
  J.P.
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Best Local
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                                                                                                                        SEQUENCE
                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                           DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                         PDB; 1VVC; 03-DEC-97.
PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M22812; AAA69605.1; --
EMBL; M35027; AAA47997.1; --
PIR; A31005; WMVZSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X13166; CAA31564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENT ACTIVATION.";

J. MOI. Biol. 272:253-265(1997).

-I. FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

-I. SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (BCA).

-I. SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                             REPEAT
20 SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                          40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiles A.P., Shaw G., Bright J., Perczel A., Campbell I.D Barlow P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody-dependent complement-enhanced neutralization of infectivity and contributes to virulence."; Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "NMR studies of a viral protein that mimics the regulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 146-263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isaacs S.N., Kotwal G.J., Moss B.;
"Vaccinia virus complement-control protein prevents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goebel S.J., Johnson G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoletti E.;
"The complete DNA sequence of vaccinia virus.";
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92115714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLETE GENOME
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                             Repeat; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97446168
                                                              Conservative
                                                                          19.3%;
                                                                                                                   28629 MW;
                                                                                                                                                                                                                                                                                                                                            3D-structure.
                                                                          Score 303; DB 1;
Pred. No. 1.82e-52
                                                              28;
                                                                                                                                            SUSHI 1.
SUSHI 2.
SUSHI 2.
SUSHI 3.
SUSHI 4.
BY SIMILARITY
                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perkus M.E.,
                                                                                                                                                                                                                                                                                                            COMPLEMENT CONTROL PROTEIN.
                                                                                                               E4322CC9A6EF8997 CRC64;
                                                                                                                                                                                                                                                                                               X SUSHI (SCR) REPEATS
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davis S.W., Winslow J.P.,
                                                                                   Length 263;
                                                        Indels 18;
                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEM3_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weller A., Isenmann S., Vestweber D.; "Cloning of the mouse endothelial selectins. Expression of both E-and P-selectin is inducible by tumor necrosis factor alpha."; J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q01102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92345617.
Sanders W.E. Jr., Wilso
"Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 92340571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamm
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELP
                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
MGD; MGI:98280; SELP.
PRINTS; PRO0343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGR_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 SPDVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                  EMBL; M72332; AAA37712.1; -. PIR; A42755; A42755.
                                                                                                                                                                                                                                             EMBL; M87861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OG 80:795-800(1992).

FUNCTION: CA(2+) DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS FUNCTION: CA(2+) DEPENDENT RECEPTOR FOR MYELOID CELLS THE TO CARROHYDRATES ON NEUTROPHILS AND MONCOYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X. SUBCELLULAR LOCATION: TYPE I MEMBERANE PROTEIN.

TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WELHEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO THE CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP
                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                         P16109; 1FSB
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                                                                                                                                                                                                                                                AAA40008.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on R.W., Ballantyne C.M., Beaudet A.L.; analysis of in vivo expression of murine P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Cell adhesion; Transmembrane;
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PFAM; PF00059; lectin_c; 1.
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TEM3_RAT STANDARD; PRT; 768 AA.

p98106;
p01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
p-setlectin precursor (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                                                                                                                     277 HPIAAFAYDSSCKFECQPGYRARGSNTLHCTGSGQWSEPLPTCEAIACEPPEIPIHGS
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Pred. No. 1.82e-52;
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A -> E (IN REF. 2).
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                                                                                                                                                                                    46;
                                                                                                                                                                                                      Length 768;
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PROSITE; PS01186; EGF 2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PFAM; PF00059; lectin_c; 1.

PFAM; PF00084; sushi; 8.

Cell adhesion; Transmembrane; Glycoprotein;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION: CA(2+) -DEPENDENT RECEPTOR FOR MYELOID CELLS THE TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LICAND RECOGNIZED IS SIALYL-LEWIS X.

-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-! TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN, LUNG, BRAIN, LUYER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.

-! INDUCTION: ACUTE INFLAMATION (PROBABLY).

-! SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

-! SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-! SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE NUMBER OF ACTIVATIONS BY SUSHI (SCR) REPEATS;
                                                                                                                                                                                                                                                                                                                                         REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, sequence comparison and in vivo expression encoding rat P-selectin.";
Gene 145:251-255(1994).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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SUSHI 1.
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C-TYPE LECTIN (SHORT FO
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01-APR-1993 (Rel. 25, C
01-APR-1993 (Rel. 25, L
15-JUL-1999 (Rel. 38, L
BETA-2-GLYCOPROTEIN I P
Kristensen T.;
"Structure of the human beta-2-glycoprotein I gene.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARC
                                                                                                              MEDLINE; 94242017.
Sellar G.C., Steel D W
                                                                         "Characterization, expression and evolution of mouse bewa glycoprotein I (apolipoprotein H)."; glycohem. Biophys. Res. Commun. 200:1521-1528(1994).
                                                                                                                                                                                                                                        APOH ON L...
MUS MUSCULUS (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Futheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                            SEQUENCE FROM N.A. STRAIN=BALB/C; TIS
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APOH OR B2GP1.
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"Molecular cloning of I
gene to chromosome 11.
                                                                                                                                                                                                                                                                                                                                                                 APOH_MOUSE
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                                             TISSUE=LIVER;
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                                                                                                                                                                                            , Shiroishi T., Moriwak K., Natsuume-Sakai S.; mouse beta 2-glycoprotein I and mapping of th
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Last annotation update)
PRECURSOR (APOLIPOPROTEIN H)
TEIN) (APC INHIBITOR) (B2GPI).
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ENDOCYTOSIS SIGNAL
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CRC64;
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EMBL; S70439;
EMBL; Y11356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIGNAL 1
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                                     p16581; p16111;
01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                     ELAM-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:88058; APOH.
                                                                                                                                                                                                                                                                                                                                                                                              SYDPGEQIVYSCKPGYVSRGGMRRFTCPLTGMW-PINTLR-CVPRVCPFAGILENGIVRY
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                                                                                                                                                                                                         VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP
                                                                                                                                                                                                                                                                                  TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                     TS---FEYPKNISFACNPGF-FLNGTSSSKCTEEGKWSPDIPACARITCPPPPVPKFALL 153
                                                                                                                                                                                                                                                                                                                                                           TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                   (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NBMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA00945.1; -. AAB30789.1; -.
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                                                                                                                                   STANDARD;
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BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 297; DB 1;
Pred. No. 7.31e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Mismatches
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SUSHI
SUSHI
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                                                                                                                                     PRT;
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                                             ADHESION MOLECULE 1)
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A MEDIANE; 3910-3000.

A YE S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupt Per C.D., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupt Per C.D., German C.D., Company and C.D., Company C.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
Phillips
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Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B. "Endothelial leukocyte adhesion molecule 1: an inducible neutrophils related to complement regulatory proteins and Science 243:1160-1165(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins T., Williams A., Johnston G.I., Gimbrone M.A. Jr., Bevilacqua M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasek M., Pittack C.,
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Hakomori S., Paulson J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 91115870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wenzel K., Felix S., Kleber F.X., Brachold R., Menke Schulte K.L., Glaser C., Rohde K., Baumann G., Speer "E-selectin polymorphism and atherosclerosis: an asso hum. Mol. Genet. 3:1935-1937(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li. Huang K.-S., Presky D.H., Familletti P.C., Wolitzky B.A., Bu. "Insight into E-selectin/ligand interaction from the crystal structure and mutagenesis of the lec/EGF domains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and chromosomal location leukocyte adhesion molecule 1."; J. Biol. Chem. 266:2466-2473(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lobb R
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ligand, sialv1-Lex.":
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c. Natl. Acad. Sci. U.S.A. 87:1673-1677(1990).
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250:1130-1132(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nudelman E., Gaeta F.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rumberger J.M., Li S., , Wolitzky B.A., Burns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCarthy K., Hopple
                                                                                                                                                                                                                                                                        ENDOTHELIAL CELLS
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PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PFAM; PF00008; EGF; 1.
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SIMILARTY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD62E entry;
WMM-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62e.htm".
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M61895, AAA52375.1;
M61888, AAA52375.1;
M61888, AAA52375.1;
M61890, AAA52375.1;
M61891, AAA52375.1;
M61892, AAA52375.1;
M61892, AAA52375.1;
M61892, AAA52376.1;
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A35046; A35046.
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                                                                 Kato H., Enjyoji K.-I.;
"Amino acid sequence and location of the disbeta 2 glycoprotein I: the presence of five Biochemistry 30:11687-11694(1991).
                  SEQUENCE OF 20-41.
MEDLINE; 90226328.
                                                                                                                                                                                                     "Complete primary structure of bovine beta localization of the disulfide bridges."; Biochemistry 31:3611-3617(1992).
                                                                                                                                                                                                                                                                       MEDLINE; 92232647.
Bendixen E., Halkier T.,
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Appella E., Kunos G
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CARBOHYD
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Pred. No. 3.95e-51
33; Mismatches 79
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                                                                                 disulfide bonds in ive Sushi domains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erythroid cells.";
Biochem. J. 267:261-264(1990)
                                                                                                                                       CONFLICT
                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation
                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                         CONFLICT
153 LSVYKPLAGNNSFYGSKAV-FKCLPHHAMFGNDTVTCTEHGNWT-QLPECREVRCPFP 208
                                                                        39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXYRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.

TISSUE SPECIFICITY: PLASMA.
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                   80
                                   97
                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL; L07303; AAA30382.1; -
IL; X60065; CAA42669.1; -
C; S23597; NBBO.
C; S09032; S09032.
                 RTYEPGEQIVFSCQPGYVSRGGIRRFTCPLTGLW-PINTL-KCMPRVCPFAGILENGTVR 96
                                   YT---TFEYPNTISFSCHTGFYLKGASSAK-CTEEGKWSPDLPVCAPITCPPPPIPKFAS 152
                                                     QTYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on from fetal bovine serum of an apolipoprotein-H-like which inhibits thymidine incorporation in fetal calf
                                                                                                    Similarity
                                                                                                                               345
                                                                                                                                                Conservative
                                                                                                                               A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                    18.6%;
                                                                                                                               38252 MW;
                                                                                                                                                                                                                                                                                                                                                                                 4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
                                                                                                            Score
                                                                                           36;
                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                         MODIFIED-SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                               BETA-2-GLYCOPROTEIN I
                                                                                                                                        HXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasma; Repeat; Sushi;
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                                                                                                                                E117DAB609461C33 CRC64;
                                                                                           Mismatches
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No. 1.
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(IN REF. 1).
(IN REF. 1).
(IN REF. 3).
(IN REF. 1).
                                                                                                    DB 1;
.57e-49;
                                                                                                             Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medof M.E., Lublin D.M., Holers V.M., Ayers D.J., Getty R.R., Leykam J.F., Arkinson J.P., Tykocinski M.L.; "Cloning and characterization folDNAs encoding the complete sequence of decay-accelerating factor of human complement."; Proc. Natl. Acad. Sci. U.S.A. 84:2007-2011(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of decay-accelerating factor suggests novel to generate two proteins.";
Nature 325:545-549(1987).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P08174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 6-381 FROM N.A. (DAF-2 FORM). MEDLINE; 87175602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nussenzweig V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caras I.W.,
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                                                                                                                                                                                                                                                                                                                 "Complete determination of disulfide bonds leconsensus repeat units of decay accelerating Biochim. Biophys. Acta 1116:235-240(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Glycophospholipid membrane anchor attachment. the cleavage/attachment site.";
J. Biol. Chem. 266:1250-1257(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91291869.
Nakano Y., Sugita
                                                                                                                        "Decay-accelerating factor CD55 is identified as the receptor for echovirus 7 using CELICS, a rapid immuno-focal cloning method."; EMBO J. 13:5070-5074(1994).
                                                                                                                                                                                                   Ward T., Pipkin P.A., Clarkson N.A.,
Almond J.w.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moran P., Raab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91093238.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakano Y., Sugita Y., Ishikawa Y., Choi N.-H., Tobe T., Tomita N
"Isolation of two forms of decay-accelerating factor (DAF) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-URINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
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                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                 FUNCTION AS A ECHOVIRUS RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                               Nakano Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
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Lublin D.M., Mallinson G., Poole J.,
Ferdman B.R., Telen M.J., Anstee D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Characterization
                                                  MEDLINE;
                                                                           VARIANT BLOOD GROUP DR(A-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I-VSSAMEPDREYHFGQAVRFYCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP
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                                                                                                                                                                                                                                                              95045399
                                                                                                                                                                                                                                                                                                                                                            Sumida K., Kikuta N., Miura N.-H., Tobe T., Tomita M.; determination of disulfide bonds localized within the short repeat units of decay accelerating factor (CD55 antigen).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davitz M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN SUSHI DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acta 1074:326-330(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kohr W.J., Caras I.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decay-accelerating factor gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhee L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88:4675-4679(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weddell G., Martin D.W. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
     Reid M.E., Thompson ., Tanner M.J.A.;
                                                                                                                                                                                                                                   Stone D.M., Minor P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomita M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysis
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                                'n
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PFAM; PF00084; sushi; 4.
Complement pathway; Plasma; Glycoprotein;
Alternative splicing; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M31516; AAA52169.1; -. EMBL; M30142; AAA52168.1; -. EMBL; M15799; AAA52170.1; -. EMBL; M64653; AAA52170.1; -. EMBL; M64356; AAA52170.1; JOINED. EMBL; S72858; AAC60633.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of reduced or absent expression of decay accelerating factor in Cromer blood group phenotypes."; Blood 84:1276-1282(1994).

-i- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION. INTERPRACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES OF THE COMPLEMENT CASCADE.

-i- FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).

-!- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT HOMODIMER (MINOR FORM).
                                                                                                                                                                                                                                   t; A39101; A39101.
t; S23138; S23138.
sP; P08603; 1HCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: THE SER/THR RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.

POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP
SYSTEM: IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CR(A),

TC(A), DR(A), ES(A), WES(B), UMC, AND IFC) AND LOW-INCIDENCE
(TC(B), TC(C), AND WES(A)) ANTICENS THAT RESIDE ON DAF. IN THE
CROMER PHEMOTYPES DR(A-) AND INAB THERE IS REDUCED OR ABSENT
EXPRESSION OF DAF, RESPECTIVELY: IN THE CASE OF THE DR(A-)
PHEMOTYPE, A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS
FOR TWO CHANGES: A SIMPLE AMINO ACID SUBSTITUTION THAT IS THE
BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING
EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
PHEMOTYPE UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
PHEMOTYPE UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
PHEMOTYPE UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
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PHEMOTYPE UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA COMPLEMENT PROTEINS. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS LINING EXTRACELLULAR COMPARTMENTS, AND VARLANTS OF THE MOLECULE ARE PRESENT IN BODY FLUIDS AND IN EXTRACELLULAR MATRIX. DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE ACTIVE SITE ON SCR3 (BY SIMILIARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR. ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHENOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RCA) FAMILY
                                                                                                          group antigen.
                                                                                                                                                                                                                                                                                        S16187.
A39101:
COMPLEMENT DECAY-ACCELERATING FACTOR REMOVED IN MATURE FORM.
4 X SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF
                                                                                                                          Membrane; Repeat;
Sushi; Polymorphism;
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RESULT
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Best Local
Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.; "Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein."; Biochem. Biophys. Res. Commun. 165:138-144(1989).
                                                                                                                                                                                                                                                                                                                P04003;
23-OCT-1986 (Rel. 02, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
                                                                                                  MEDLINE; 90073699.
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominida
                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                            C4BPA OR C4BP.
                                                                                                                                                                                                                                                                                                      C4B-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                     C4BP_HUMAN
                                                                                                                        FISSUE=LIVER;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                               (Rel. 35, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 293; DB 1;
Pred. No. 8.51e-50;
43; Mismatches 75
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R -> L (IN TC(B) ANTIGEN).

/FTId=VAR_001997.

R -> P (IN TC(C) ANTIGEN).

/FTId=VAR_001998.
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S -> M (IN REF. 2).
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HTCFTLTGLLGTLVTMGLLT -> SRPVTQAGMRWCDRSSLQSRTPGFKRSFHFSLPSSWYYRAHVFHYDRFAWDASNHGLA
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SUSHI 2.
SUSHI 3.
SUSHI 4.
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/FTId=VAR_002000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_001999
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                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                   597
                                                                                                                                                                                                          Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 381;
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SEQUENCE FROM N.A.
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Dahlback B., Smith C.A., Mueller-Eberhard H.J.;

Pulsualization of human C4b-binding protein and its complexes with vitamin K-dependent protein S and complement protein C4b.";

PIOC. Natl. Acad. Sci. U.S.A. 80:3461-3465 (1983).

-i- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT C4B. I BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR C4B. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic organization of the alpha chain of the human C4b-binding protein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chung L.P., Gagnon J., Reid K.B.M.; "Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and malignment of the fragments produced by limited
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 203-288 FROM N.A. MEDLINE; 86301119. Lintin S.J., Reid K.B.M.; "Studies on the structure of the FEBS Lett. 204:77-81(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4b-binding protein and interspecies cDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteolysis with chymotrypsin and the peptides produced by cyanogen
bromide treatment.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Derivation of the sequence of the signal peptide in human C4bp C4b-binding protein and interspecies cross-hybridisation of the C4bp
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 49-88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lintin S.J.,
                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, AND LIGAND BINDING MEDLINE; 83221615.
EMBL; M31452; AAA36507.1; -. EMBL; M62486; AAA36506.1; -.
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                                                                                                                                                                                                                                                                                                                              (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BCA COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SEROM AMYLOID P COMPONENT.

SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OF 3 POSSIBLE SORTS: A 570 KD COMPLEX OF 7 ALPHA CHAINS AND 1 BET CHAIN, A 530 KD HOWOHEPTAMER OF ALPHA CHAINS OR A 570 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CHAIN SOR A 570 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CHAIN SOR A 570 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CHAINS OR A 570 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CHAINS OR A 570 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CHAINS OR A 570 KD COMPLEX OF 6 ALPHA CHAIN SON A DETA CHAIN. THE CHAINS OR A 570 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CHARACTER OF A CHAIN THE END.
                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
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182 RNGR--HSG-E-ENFYAYGESVTYSCDPRFSLLGHASISCTVENETIGVWRPSPFTCEKI
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X04296;
X02865;
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M62485;
X07853;
                                              FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYR-EC-DTD-GWTNDIPICEVVKCLPVTAP
                                                                                                                                         TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 123
                                                                              VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI
                                                                                                              SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT
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                                                                                                                                                                                                                                                                                                          pathway;
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Pred. No. 5.35e-49;
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EMBL; X64346; CAA45627.1; -
EMBL; X60283; CAA42823.1; -
EMBL; X60283; CAA42822.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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"New member of the multigene
herpesvirus saimiri.";
J. Virol. 66:3937-3940(1992).
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                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Albrecht J.-C., Nicholas J., Biller D., Camero Newman C., Wittmann S., Craxton M.A., Coleman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENT CONTROL PROTEIN HOMOLOG 4 OR CCPH.
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J. Virol. 66:5047-5058(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Viruses; dsDNA viruses, no RNA stage;
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SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).
SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                        Repeat; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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  Transmembrane; Alternative splicing;
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oleman H., Fleckenstein B.,
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Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-FEB-1996 (Rel. 33, Last anotation update)
Q1-FEB-1996 (Rel. 33, Last anotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
                                                                                                                                                                                                                                                                                    Weller A., Isenmann S., Vestweber D.;

"Cloning of the mouse endothelial selectins. Expression of both E and P-selectin is inducible by tumor necrosis factor alpha.";

J. Biol. Chem. 267:15176-15183(1992).

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Murine endothelial leukocyte-adhesion molecule 1 is a close structural and functional homologue of the human protein."; Eur. J. Biochem. 206:401-411(1992).
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
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NO. 1.82e-48;
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Best Local
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PROSITE; PS00022; EGE_1; 1.
PROSITE; PS01186; EGE_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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                                                                 242 ECEALT-HPAHGIRKCSSNPGSYPWNTTCTFDCVEGYRRVGAQNLQCTSSGIWDNETP-- 298
358 PQIPVCKAVQCEALSAPQQGNMKCLPSASGP-FQNGSSCEFSCEEGFELKGSRRLQCGPR 416
                                  299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M87862;
                                SCKAVTCDAIPOPONGFVSCSHSTAGELAFKSSCNFTCEOSFTLQGPAQV-ECSAQGOWT 357
                                                  DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00084;
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                 KCQKRPCGH-P-GDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                    49;
                                                                                            Similarity
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                                                                                   Conservative
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                                                                                            18.3%;
25.1%;
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C-TYPE LECTIN (SHORT FC
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. 1.82e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                       (SHORT FORM)
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM.1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSEDIOOM C.L., Auchampach J.A., Anderson D.C., Manning A.M.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
-i- EMBLARES THEIR BINDING TO LEUKOCYTES. THE LICAND RECOGNIZED BY
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELE OR ELAM-1
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                          DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00084; sushi; 5. Cell adhesion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00022; EGF_1; 1.

PROSITE; PS000615; EGF_2; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1;

PROSITE; PS50041; C_TYPE_LECTIN_2;
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SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
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C-TYPE LECTIN (SHORT FORM).
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Search completed: Thu Jun 8 21:38:24 2000 Job time: 12 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.2%; Score 286; DB 1; Length 549; Best Local Similarity 25.1%; Pred. No. 6.17e-48; Matches 50; Conservative 45; Mismatches 97; Indels
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CARBOHYD
                                                              418 EWDSEKPTCAGVQCSSLDL 436
| || || || || 1
179 FWSKEKPKCVEISCKSPDV 197
                                                                                                                          242 ECKALTQPAHG-VRKCSSNPGSYPWNTTCTFDCEEGYRRVGAQNLQCTSSGVWDNEKPSC 300
                                                                                                                                                           359 QIPVCKASQCEALSAPQRGHMKCLPSASAP-FQSGSSCKFSCDEGFELKGSRRLQCGPRG 417
                                                                                                                                                                                                                                             301
                                                                                                                                                                                              61 KCQK-RPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYOLLGEINYRECDTDG-WTN 118
                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                    KAVTCDAIPRPQNGSVSCSNSTAGAL-AFKSSCNFTCEHSFTLQGPAQV-ECSAQGQWTP 358
                                                                                                                                                                                                                                                                  DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
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549 AA;
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60079 MW;
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Release 3.1A John F. Collins, Biocomputing Research Unit-copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jun 8 21:37:08 2000; MasPar time 8.38 Seconds 585.300 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-316-163-9 (1-207) from US09316163.pep 1573

Sequence: 1 EDCNELPPRRNTEILTGSWS......VEISCKSPDVINGSPISQKI 207

Scoring table: PAM 150

Gap 11

188963 seqs, 23686106 residues

Database:

Post-processing: Minimum Match 0% Listing first 45, ∦geneseqp éseq36 /summaries

Variance 114.255; scale 0.273

Statistics:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	Çī	4	ω	2	ъ	Result No.
288	288	290	293	293	293	293	293	293	293	293	293	293	293	298	298	298	298	298	308	308	842	973	Score
18.3	18.3		18.6		18.6	•	18.6	18.6	8	m	18.6	18.6	18.6	m	ന	æ	œ	18.9	19.6	19.6	53.5	\vdash	Query Match
302	302	581	577	440	440	440	440	381	381	381	381	381	299	610	610	610	610	610	830	484	216	240	Length
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R55793	W26320	R13490	W06882	R66684	P70049	W27483	P94774	W73505	P94773	P70048	R66683	W26317	W06881	W46733	W18839	R05538	R05494	R08116	R65216	W99892	W39155	W39154	ID
	Herpesvirus secreted g	Human C4 binding prote	Membrane co-factor pro		н	Human glycophosphatidy	Membrane bound decay a	elerating ra		н	Decay accelerating rac	н	Decay accelerating fac	ന	•	Endotherral-reukocyte	Endotherial Teukocyce			Porcine E-selectin.		=	Description
1.71e-19	1./1e-19	1.04e-19	4.966-20	4.95e-20	4.906-20	4.906-20	4.966-20	, ,	* 900	4.96e-20	4.968-20	4.956-20		1.456-20	1.400-20	1.430-20	1.436.20	1.450-20	1.198-21	1.196-21	1 100 01	•	Pred. No.

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121 INGSPISQKI 130

44 45	43	42	41	40	39	38	37	36	ယ Մ	34	33	32	31	30	29	28	27	26	25	24
273 273	275	275	276	276	276	276	276	279	278	278	278	281	281	281	281	281	284	286	288	288
17.4 17.4	17.5	17.5	17.5	17.5	17.5	17.5	17.5	17.7	17.7	17.7	17.7	17.9	17.9	17.9	17.9	17.9	18.1	18.2	18.3	18.3
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CD46 from clone pm5.10		CD46 construct subSCR2	3	rsMCP protein SEQ ID N		co-tactor	Membrane cofactor prot	Porcine P-selectin.	CD46 from clone pmb.1.	from clone	from clone pm	n membrane cora	Human CD46.	CD46 CONSTRUCT SAUSCRO		CD46 WIId-type.	Porcine comprement in	۲	h F	membrane
6.95e-18	4.25e-18	. 25e-			3 6	3.526-10	3.326-10	1.30e-10	1.05e-10	2.03e-10	2.03e-10	9.00E-19		0.000		9.000 10	0 660-10	4 KOD-19	3 919-10	1.71e-19

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06-MAR-1997; US-81281.
09-APR-1996; US-015083.
09-APR-1996; US-630048.
06-MAR-1997; US-038814.
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W39154 standard; Protein; 240 AA.

W39154;
W39154;
27-APR-1998 (first entry)
Human partial Complement factor H protein fragment 1.

Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This partial protein sequence represents a region of the human tumour-associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens isolated from clone pRBB9FH410 (see W39155). The detection of such proteins and a CFH antigens can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BARD-) BARD DIAGNOSTIC SCI INC.
Enfield DL, Hass GM, Kinders RJ;
WPI; 97-512742/47.
N-PSDB; V02790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Factor H related antigen, or nucleic acid encoding it Example 6B; Fig 6B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            urogenital cancer; medicament; modulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
138 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                   7 Match 61.9%;
Local Similarity 100.0%;
hes 130; Conservative
                                          61 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 120
                                                                                                                                                         240 AA;
                                                                                                                                                                                                                                                                                                                                Score 973; DB 1; Length 240; Pred. No. 6.80e-97; 0; Mismatches 0; Indels
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198 INGSPISOKI 207

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Best Local :
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09-APR-1997; US-812481.

09-APR-1996; US-015083.

09-APR-1996; US-630048.

06-MAR-1997; US-038614.

06-MAR-1997; US-038614.

(BARD-) BARD DIAGNOSTIC SCI INC.
Enfield DL, Hass GM, Kinders RJ;
WPI; 97-512742/47.
                                    The present sequence is porcine E-selectin (E-sel). The nucleotide sequence encoding E-sel may be used in the diagnosis, prevention and treatment of tissue rejection following xenotransplants of pig organs and also in the monitoring (by specific measurement of the amount of
                                                                                                                                                          Nucleic acids encoding the porcine E-selectin protein - useful diagnosing and treating rejection of xenotransplanted pig organs Claim 1; Column 47-50; 30pp; English.
                                                                                                                                                                                                                                                                                                 (ALEX-) ALEXION PHARM INC.
Evans MJ, Matis LA, Rollins S, Rother RP;
WPI; 99-253853/21.
                                                                                                                                                                                                                                                                                N-PSDB; X19809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine; E-selectin; diagnosis; transplant rejection; xenotransplant; cytokine; donor organ endothelium; inflammatory cell; graft tissue; acute cellular allograft rejection; cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994; 252493.
01-JUN-1994; US-252493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5891645-A.
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Example 6B; Fig 6B; 104pp; English.

This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer agents that may modulate this antigen could be used in the manufacture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine E-selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W99892 standard; Protein; 484
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by modulating or detecting tumour associated human complement Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V0279;
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Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urogenital cancer; medicament; modulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ 154
in the blood of the patient) and modulation of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 53.5%;
Similarity 99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for the treatment of a tumour cell.
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Pred. No. 8.32e-82;
""smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 216;
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61 KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117

QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313

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                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                  P-selectin gene - for regulating gene expression in engotherial cells and mega:karyocyte(s) bisclosure; Fig 1; 88pp; English.

The sequence is that of the P-selectin gene product from endothelial cells, determined from a composite of four overlapping cDNAs: lambda GMPE1-lambda GMPE4. The P-selectin gene or its fragments may be used GMPE1-lambda GMPE4. The P-selectin gene or its fragments may be used
                                                                                                                                                                             Sequence
                                                                                                                                                                               bacterial sepsis, tumour metastases, atherosclerosis, Sequence 830 AA;
                                                                                                                                                                                                            to inhibit P-selectin expression, thus controlling inflammatory and haemostatic processes in e.g. rheumatoid arthritis, ischaemic injur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endothelium, contributes to the binding and subsequent transmigration of inflammatory cells into the graft tissue that occurs during acute cellular allograft rejection. Therefore, preventing expression of E-sel on the donor tissue may reduce the risk of rejection by modulating E-sel mediated cell adhesion. Fragments of the nucleotide sequence encoding E-sel may be used as polymerase chain reaction (PCR) primers or hybridization probes for the identification and/or isolation of the porcine E-sel gene from genomic DNA. Antisense sequences may be used to inhibit the expression of E-sel. DNA constructs may be used to introduce antisense sequences to a cell, or to inactivate the E-sel gene (e.g. knock-out constructs). Cells in which the expression of E-sel has been prevented may be used as disease models or to produce transplantation with
                                                                                                                                                                                                                                                                                                                                                          Expression control elements in the 5'- flanking region of the P-selectin gene - for regulating gene expression in endothel
                                                                                                                                                                                                                                                                                                                                                                                                               Mcever RP, Pan J; WPI; 95-106847/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1994; 009395.
20-AUG-1993; US-110158.
(OKLA ) UNIV OKLAHOMA STATE.
MCEVER RP, Pan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R65216;
04-OCT-1995
                                     199 ECGELELPQHV-LMNCSHPLGNFSFNSQCSFHCTDGYQVNGPSKLECLASGIWTN-KP-P 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Control elements; gene expression; endothelial cells; megakaryocytes; rheumatoid arthritis; ischaemic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R65216 standard; Protein; 830 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a reduced risk of rejection. Sequence 484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSSLEV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the transplants. Cytokine-induced expression of E-sel by donor organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 NHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQPKNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 TGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTYPEGTQAIYKCRPGYRSLGNVIMYC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                               h 19.6%;
Similarity 26.8%;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial sepsis; tumour metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.6%;
                                                                                           44;
                                                                                                            Score 308; DB 1;
Pred. No. 1.19e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 308; DB 1;
Pred. No. 1.19e-21;
                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                      94;
                                                                                                                              Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 484;
                                                                                  Indels 12;
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The protein possesses a hydrophobic N-terminal sequence contaracteristic of a signal sequence. It is predicted that the mature contaracteristic of a signal sequence. It is predicted that the mature contaracteristic of a signal sequence. It is predicted that the including contarged the signal sequence and is followed by a hydrophobic transmembrane contends of 24 amino acids. The protein possesses a short, charged cryoplasmic tail of 32 amino acids. It is noted that the protein contains eleven N-glycosylation sites.

ELAM can be used to identify molecules which inhibit binding of cleucocytes to cells, and such binding can be inflammation can be treated) using an ELAM (or fragment), can be used to recognise MILA, ELAM ligands or their fragments, capabohydrates which bind to ELAM and antibodies which recognise ELAM.
                                                                                                                                  Qγ
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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27-APR-1990; U02357.
28-APR-1998; US-345151.
01-JUN-1989; US-359316.
18-DEC-1989; US-452675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pSQ148 and pSQ149.

Endothelial cell-leucocyte adhesion molecule 1; ELAM1; antibodies; Endothelial cell-leucocyte adhesion; MILA; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9013300-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endothelial cell-leucocyte adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R08116 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endothelial cell adhesion mols. inhibition-detection of binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hession C, Lobb RR, Goelz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R08116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 90-361248/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1991
22-OCT-1990 (first entry)
Endothelial leukocyte adhesion molecule-1 (ELAM-1).
Endothelial leukocyte adhesion molecule; ELAM-1; inflamation;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GFWSKEKPKCVEISCKSPDV-INGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 GHWSAPLPTCEAISCEPLESPVHGS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                              R05494 standard; protein;
                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                        210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
                                                                                                                                       151
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                        AVYTCNEGYQLIGEINYRECDTDG-WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREY 150
                                                                                                                                                                                                                                    CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF
                                                                                                                                                                                                                                                                      CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
                                                                                                                                                                      TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
                                                                                                                                       HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                  610 AA;
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                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                       610
                                                                                                                                                                                                                                                                                                                                            Score 298; DB 1,
Pred. No. 1.43e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule 1 from pCDM8 clone 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benjamin
                                                                                                                                                                                                                                                                                                                                                                                Length 610;
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      injury, vasculitis etc. It may also be useful in treatment and diagnosis of leukaemia, lymphomas and metastic spread of tumour cells, as well as in mediation of cell-cell interactions in embryogenesis and organ development, in neoplasia, and wound and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in treating inflamation, post reperfusion injury, bacterial infection, vasculitis, leukaemia etc. Claim 13; 36; 54pp; English. ELAM-1 is useful in treatment of inflamation, post reper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9005786-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-1989; 005073.
14-NOV-1988; US-270873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                            adhesion protein.

Adhesion protein.

Bisclosure; 44pp; English.

BIAM specific antibodies, attached to a suitable drug eg. a

EIAM specific antibodies, attached to a suitable drug eg. a

cytotoxin can direct the action of the drug to sites of

cytotoxin can direct the action of the drug to sites of

inflammation, tissue damage and infection. The same Abs can be

inflammation, tissue damage and infection. The same abs can be

used to treat leukaemia, lymphoma, vasculitis and metastic spread

used to treat leukaemia, lymphoma, vasculitis and metastic spread

used to treat leukaemia, lymphoma, vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

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used to treat leukaemia, lymphoma; vasculitis and metastic spread

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used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; vasculitis and metastic spread

used to treat leukaemia, lymphoma; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1990 (first entry) | Endothelial-leukocyte adhesion molecule (ELAM-1). Endothelial-leukocyte adhesion molecules; ELAM-1; cytotoxin; cytokine; cancer; leukemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHO-) Gen Hospital Corp
(BRIG-) Brigham Womens Hosp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R05538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia; lymphoma; metastasis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bevilacqua Mp, Grimbrone MA; WPI; 90-193270/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
WO9005539-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R05538 standard; protein;
                                                                                                                    of cancer cells. Labelled ELAM specific Abs can be used expression of the adhesion molecules. Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                                                              and for detecting expression of this endothelial leucocyte
                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against ELAM-1 to treat inflamation, infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-1989; 005075.
14-NOV-1988; US-270860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                          leukaemia
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18.9%;
Local Similarity 27.4%;
hes 45; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRPGYRSLGNVIMVCRK-GEWVALNPLRKCOKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes expressing endothelial-leukocyte adhesion molecule-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 27.48
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q04776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610 AA;
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27.48;
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Pred. No. 1.43e-20
                Score 298; DB 1;
pred. No. 1.43e-20;
33; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed B,
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                                                                     Length 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
W46733 standard; Protein; 610 AA W46733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is E-selectin (formerly known as endothelial leukocyte adhesion molecule-1; EIAM-1). E-selectin is identified by specific binding of murine monoclonal antibodies H4/18 and H18/7, developed against stimulated endothelial cells. New immunoconjugates of the invention comprise monoclonal antibody H18/7, or a fragment which binds to E-selectin conjugated to a therapeutic agent. The immunoconjugate is used to selectively target the therapeutic gent to activated endothelium expressing E-selectin, especially for treating inflammation, microbial infections, post-reperfusion injury, malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or acute or chronic allograft rejection. Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-selectin; endothelial leukocyte adhesion molecule-1; ELAM-1; murine monoclonal antibody; H4/18; H18/7; immunoconjugate; activated endothelium; treat; inflammation; microbial infection; post-reperfusion injury; malignant tumour; vasculitis; vascular smooth-muscle cell proliferative disorder; acute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumours, vasculitis, vascular smooth-muscle cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immuno:conjugates based on monoclonal antibody specific E-selectin - for targetting therapeutic agent to activate
                                                                                                                                                                           151
                                                                                                                                                                                                                          326 TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endothelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T70493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Column 35-38; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gimbrone MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1994; US-365470.
14-NOV-1988; US-270860.
13-MAR-1992; US-850802.
05-AUG-1993; US-102510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                             268 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-selectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
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                                                                                                                                                                                                                                                                                            AVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREY
                                                                        φ
                                                                                                                                                                HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 298; DB 1;
Pred. No. 1.43e-20;
33; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 610;
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Best Local
                                                                                                                                                                               Homo sapiens. W09634965-A2. 07-NOV-1996.
                                                       Chimeric proteins for inhibiting complement-mediated cell lysis
                                                                                                                                                                                                                                             Complement inhibitor; membrane co-factor protein; MCP; decay accelerating factor; DAF; chimeric protien; glycosaminoglycan; heparin; cell lysis; sepsis; adult respiratory distress; syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents human endothelial leukocyte adhesion molecule-1 (ELAM-1). ELAM-1 is a membrane glycoprotein which is induced by a number of cytokines. Pathological conditions associated with the overexpression of cellular adhesion molecules, such as ELAM-1 or intracellular adhesion molecule-1 (ICAM-1), can be treated with the novel pharmaceutical composition of the invention. The composition comprises an effective amount of an ICAM-1 antisense molecule encapsulated in a lipid mixture, the lipid mixture comprising at cationic lipids. The composition is used in a method to treat pathological conditions associated with overexpression of ICAM-1, such as Alzheimer's disease, multiple sclerosis, viral hepatitis,
peptide sequences
Disclosure; Page 25; 33pp; English.
                                         comprise membrane co-factor protein
                                                                                                   (CHIR ) CHIRON CORP
Creasey AA, Innis 1
                                                                                                                                       03-MAY-1996; U06301.
05-MAY-1995; US-435149
                                                                                                                                                                                                                                     reperfusion injury; cell damage.
                                                                                                                                                                                                                                                                                                               Decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                       W06881;
                                                                                                                                                                                                                                                                                                                                                                   W06881 standard; Protein;
                                                                                                                                                                                                                                                                                                                               18-MAR-1997 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for treatment of conditions associated with overexpression of ICAM-1 - used to treat e.g. Alzheimer's disease, glomerulonephritis, rheumatoid arthritis etc. Disclosure; Pages 44-46; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1998 (first entry)
Amino acid sequence of endothelial leukocyte adhesion molecule-1.
Endothelial leukocyte adhesion molecule-1; ELAM-1; inducible; cytokine; overexpression; cellular adhesion molecule; intracellular adhesion molecule-1; ICAM-1; antisense molecule; lipid mixture; Alzheimer's disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-1996; US-657753.
(UVBR-) UNIV BRITISH COLUMBIA.
HOPE MJ, Klimuk SK, Scherrer P, Semple SC;
WPI; 98-042180/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                           151 HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholangitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; V16208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral hepatitis; cholangitis; cardiac allograft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 18.9%;
Local Similarity 27.4%;
                                                                               96-506167/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610 AA;
                                                                                                     Innis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiac allograft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                   Zaror I;
                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 298; DB 1; Le
Pred. No. 1.43e-20;
33; Mismatches 79;
                                   and decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                             194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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                                                 This protein sequence comprises human decay accelerating factor (DAF), a protein that has C3 complement inhibitor activity. Claimed retroviral vector particles express a complement inhibitor such as DAF, and are thereby protected from inactivation upon exposure to body fluids containing complement. Also claimed are: (1) a producer cell producing the vector particle; and (2) a chimeric retroviral envelope protein (see also W26326) with at least part of the N-terminal receptor-binding domain removed and replaced by a protein domain having a complement inhibitor activity. The vector is used in a claimed method for transducing cells in the presence of a body fluid containing complement, preferably ex vivo, especially the protein complement, preferably ex vivo, especially the protein containing complement, preferably ex vivo, especially the protein containing the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein acquired blood disorders by the protein contains the protein acquired blood disorders by the protein
                                                                                                                                                                                                                                                                                                                                                                                                                 Retroviral vector particle expressing complement inhibitor activity for transducing cells in body fluids containing complement Disclosure; Column 41-46; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human decay accelerating factor:
DAF; decay accelerating factor; human; C3 complement inhibitor;
retrovirus; vector; gene therapy; stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W26317 standard;
W26317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997.
21-JUL-1994;
                                  for gene therapy, e.g. of hereditary or actransduction of haematopoietic stem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T84471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mason JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALEX-) ALEXION PHARM INC.
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nes 58; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97-350243/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Squinto SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 AA;
      381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35. .381
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Sig_peptide
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Pred. No. 4.96e-20;
43; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 299
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20-DEC-1994.
02-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 95-035649/05.
N-PSDB; Q79863.
Liposome(s) for targetting particular cells contg. fusion protein of glyco:phosphatidyl:inositol anchor and heterologous targetting protein, e.g. for delivering toxins to infected or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Decay accelerating factor; DAF; mDAF; fusion protein; liposome; cell targeting; glycophosphatidylinositol; GPI; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig. 1a-1f; 36pp; English.

A probe (given in 079865) based on the N-terminal sequence of human decay accelerating factor (DAF) was used to screen a HeLa cell lambda cDNA library. Isolated clones encoding membrane-bound DAF (mDAF) were obtained, and the full sequence of mDAF cDNA was determined (079863). The GPI signal domain of mDAF may be fused to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-1986; US-859107.
06-AUG-1987; US-083757.
19-DEC-1991; US-811048.
12-FEB-1993; US-017934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                a heterologous protein and targeted to cell membrane surfaces sequence 381\ \text{AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decay accelerating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R66683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R66683 standard; Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caras IW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 VNNDEGEWSGPPPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 18.6%;
Local Similarity 29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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213 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
                                                                                                                                                                                                                                                    98 C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVE 156
                                                                                                                                                                                                                                                                                                                    Local Similarity
les 58; Conser
                                                            59 LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG- 115
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                                                                                                                        F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 212
                                                                                                                                                                                        CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENENTECH INC
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                                                                                                                                                                                                                                                                                                                       Conservative
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derivatization site"
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Pred. No. 4.96e-20;
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                     Score 293; DB 1;
Pred. No. 4.96e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                       75;
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                                                                                                                                                                                                                                                                                                                                                                                   Length 381;
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                                                                                                                                                                                                                                                                                                                       Indels 19;
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Best Local
                                                                    N-PSDB; N91043
                                                                                                                 WPI;
                                                                                                                                                 Caras
                                                                                                                                                                                                                                                                                                                                                                                                                                         Decay accelerating factor (DAF) of clones lambda DAF; allograft rejection; affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /T 14
P94773 standard; protein; 381 AA.
                                                                                                                                                                                                                  3-AUG-1988; 02648.
6-AUG-1987; US-083757.
                                                                                                                                                                                                                                                                                                   09-FEB-1989.
                                                                                                                                                                                                                                                                                                                                            WO8901041-A.
                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUL-1990 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      using recombinant DNA procedures.

Disclosure; Page 15-17; 20pp; English.
The probable phosphatidyllnositol derivatisation site is Cys(330). The DAF variant is useful for treating paraoxysmal nocturnal haemoglobinuria, or inflammatory or cell lytic autoimmune diseases. It may be used to ameliorate allograft rejection or autoimmune diseases. See also N70046, N70048.
                                                                                                                                                                                      (GETH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New decay accelerating factor variants - obtained with the factor by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 87-308481/44.
N-PSDB; N70047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1987;
02-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-244267-A.
04-NOV-1987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 --- DDGFWSKEKPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH) Genentech Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 VNNDEGEWSGPPPEC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP
                                                                                                     89-061177/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS
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            polypeptide for targeting protein to cell membrane
                                                                                                                                                                              Genetech Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 18.6%;
Similarity 29.7%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303944.
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331. .347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 293; DB 1;
Pred. No. 4.96e-20;
43; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DINA-) DINABEKKU KENKYUSHO KK WPI; 99-074147/07.
        176
                                                                                 269
                                                                                                                                                                                                                                                                                                                                                                                            157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1999 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W73505 standard; Protein; W73505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1997; 125965.
15-MAY-1997; JP-125965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 29.7%; hes 58; Conservation
                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 --- DDGFWSKEKPKC 187
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---DDGFWSKEKPKC 187
                                                                        VNNDEGEWSGPPPEC 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 AA;
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llarity 29.7%;
Conservative
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Example 3; Page 8-9; 15pp; Japanese.

This sequence is the human decay accelerating factor (DAF) protein.

DAF can be used in the viral vector of the invention. The viral vector contains a factor controlling the function of a human complement protein, particularly a membrane combining type protein. The viral vector, which is stable in situ, is useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector having complement controlling factor - useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprisesphospholipid anchor domain with heterologous polypeptide.
Disclosure; 6lpp; English.
Recombinant DAF's are useful in treatment of inflamatory or cell lytic autoimmune diseases and allograft rejection. Useful in diagnostic compositions or in affinity purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decay accelerating factor protein.

DAF; decay accelerating factor; human; compliment protein; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKJEGDEEMHCS
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                                                                                                                                                                                                                                                     3 CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREDSLSPKLTCLQNLKWSTAVE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP 58
                                                     WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
                                                                                                                                                              C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVE
WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS
                                                                                                                            LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG-
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 293; DB 1;
Pred. No. 4.96e-20;
                                                                                                                                                                                                                                                                                                                                                                                     43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 293; DB 1;
Pred. No. 4.96e-20;
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                                                                                                                                                                                                                                                                                                                                                                                        75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                  Indels 19;
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Search completed: Thu Jun 8 21:37:19 2000 Job time: 11 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:40:50 2000; MasPar time 9.79 Seconds 641.132 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: >US-09-316-163-10 (1-265) from US09316163.pep 2029 1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK 265

Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries Searched: 188963 segs 23686106 residues

Database: a geneseq36

Statistics: Mean 32.240; Variance 119.188; scale 0.271

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	21	20	19	18	17	16	15	14	. 13	12	11	10	ဖ	8	7	o	ы	4	ω	2	1	Result
330	330	330	332	332	332	333	333	335	335	335	335	335	341	341	341	341	344	371	382	1298	1429	Score
16.3	16.3	16.3	16.4	16.4	16.4	16.4	16.4	16.5	16.5	16.5	16.5	16.5		σ	16.8	16.8	17.0	18.3	18.8	64.0	70.4	Query Match
357	254	251	377	373	324	279	279	384	384	377	377	376	360	360	302	302	830	263	581	216	240	Length
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R10927	W06880	R41361	R15229	R15230	R15233	R41360	W69523	R86316	R10924	W27484	R93941	R93939	R55792	W26319	R55793	W26320	R65216	P92003	R13490	W39155	W39154	ID
Human membrane cofacto Membrane co-factor pro	Membrane co-factor pro	Membrane cofactor prot	CD46 from clone pm5.1.	from clone	from clone pmo.	rane cotactor pr			Human membrane cofacto		CD46 construct subscks	wild-type.	Herpesvirus saimiri mc	membrane	Herpesvirus saimiri sc	റ	P-selectin.	Deduced sequence of co	Human C4 binding prote	KB9FH410	-	Description
1.82e-23	٠.	· _		1.11e-23	1.116-23	0.006-24	8.58e-24	5.298-24	1 U	ιυ	5.296-24	5.298-24		1.196-24	1.19e-24	1.19e-24	5.6/e-25	6.80e-28	4.34e-29		1.09e-147	Pred. No.

	45	44	43	42	41	40	39	38	37	36	ဌ	34	<u>ω</u> ω	32	3 1	30	29	28	27	26	25	24
	318	318	318	318	318	318	319	318	321	322	323	323	324	326	327	327	328	328	328	329	329	329
	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.8	15.9	15.9	15.9	16.0	16.1	16.1	16.1	16.2					
	2039	543	543	543	543	543	543	254	543	543	543	248	326	579	350	336	2317	1930	778	378	377	290
	μ.	Н	Н	-	۰ ـ	- ب		ب	ш	۲	-	-	Н	Н	سر	μ	-بر ،	_	سا	ب.	-	Ъ
	R11810	R28571	R28570	K28569	R28566	R28552	R28550	715	R28560	R28557	R28553	R74999	R74998	W39924	R15231	R15232	P92219	W45899	W73147	R93940	R93942	W39156
	Human complem	CR1-4 (364-36/	-4 (250		- 4 (UEOS)	4 (701,	-4 (54K)	nce or	(114S)	-4 (99H,	(858,	beta-2	Human beta-2	Amino acid se	CD46 from Clone		.0	5	Amino acid sec	CD46 CONSCIUCE SUBSCIA		n partial
•	comprement type	/ NAAn) a	717171		- 1	310N) and to	analogue.	soluble co	analogue.	IUSE) anai	8/N) analo	grycoprot	beta-2 grycoproc	sequence or	curd	ית הית) 3 7	complement recep	acid sequence of	C SUDSCAL	C SUDSCAS	compleme
	0.000-66	0. CUC		.:		. :	3 530-33	100	. 000	.000	1.000-22	. 000-2	0000	1000	000		שנים שנים	.996-2	200	9.	320	ພິພ ຍິຍ

ALIGNMENTS

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U9-APR-1996; US-012481.

PR 09-APR-1996; US-015083.

PR 06-MAR-1997; US-030648.

PA (BARD-) BARD DIAGNOSTIC SCI INC.

'I Enfield DL, Hass GM, Kinders RJ;

RWPI; 97-512742/47.

Treating or free ting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                  region
                                                                                                 region
                                                                                                                                               protein
                                                                                                                                                                                                                                                  C4bp; monomer; complement protein; pJOD.C4bp.3; SCR; short consensus repeat.
                                                                                                                                                                                                                                                                                                                                R13490;
30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H related antigen, or nucleic acid encoding it

Example 6B; Fig 6B; 104pp; English.

This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                   Human C4 binding protein
                                                                                                                                                                                                                                                                                                                                                                    T 3
R13490 standard; Protein; 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1998 (first entry)
Clone pRRB9FH410 CFH related protein fragment.
Complement factor H; tumour associated antigen; renal cancer;
urogenital cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Fact H related anticen. or nulsic and associated human complement Fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W39155 standard; Protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9738136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AVRFYCNSGYKIEGDEEMHCSDDGFWGKEKPKGVEISCKSPDVINGSPISQKIIYKENER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 medicament for t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 TCNEGYQLIGEINYREGOTDGWTNDIPICEYVKCLPVTAPENGKIVSSAMEPDREYHFGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCNEGYQLLGEINYRECDTDGWTNDIPICEYVKCLPYTAPENGKIVSSAMEPDREYHFGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQYKCNMGYEYSERGDAYCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYSPLRIK 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.08;
L Similarity 99.48;
170; Conservation
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                /label = SCR8
94. .155
                          /label- SCR7
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                  /label= C4bp
                                                                                                                                                           /label= signal_peptide
                                                                                                                                            . 581
                                                                                              . 93
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Pred. No. 1.28e-132;
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PT New C4 binding protein fusion proteins and DNA encoding them comprise assemblies of C4bp monomers linked to functional moiety, PT comprise assemblies of C4bp monomers linked to functional moiety, PT e.g. A2T, useful as delivery vehicles in diagnosis and therapy CC containing 1; Fig 1; 105pp; English.

CC This sequence was deduced from human hepatocyte (Hep G2) cDNA cobtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCR, CC the first cysteine residue bonds with the third and the second cysteine residue bonds with the third and the second cysteine residue bonds with the fourth. This secondary structure is cresponsible for the conformational flexibility of the C4bp monomer. CC The invention covers fusion proteins in which the monomer sequence, is fused to the C-terminal of a protein such as a viral receptor, cell ligand, a bacterial, viral or parasitic immunogen, enzyme, cc cytokine. toxin. erg. Sepa also 11324.51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
P92003 standard; protein; 263 AA
                                                                                                 248 SCDN-PYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                          282 SCINLPDIPHA 292
                                                                                                                                                                                             191
                                                                                                                                                                                                                        222 TCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEPN 281
                                                                                                                                                                                                                                                                        135 ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-D-D--GFWSKEKPKCVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOG-) BIOGEN INC.
Pasek MP, Winkler G, Liu TR;
WPI; 91-252613/34.
                                                                                                                                                                                                                                                                                                                 166 RNGR--HSG-E-ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI 221
                                                                                                                                                                                                                                                                                                                                                                                                           108 VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1991;
26-JAN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 TETREKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 79; Conser
                                                                                                                                                                              SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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65. .92
/note=
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.e= "intradomain"
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el= SCR4
.406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 382; |
Pred. No. 4.:
52; Mismatcl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
.34e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 581;
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Best Local
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20-AUG-1988;
20-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein with anti-complement activity
- encoded by Vaccinia virus 35K gene
Disclosure; Figure 2A, 20pp; English.
C4b-binding protein which specifically blocks human complement cascades.
It is the deduced sequence of a 35kDa protein encoded by sequence 52-840
of the 35K gene of vaccinia virus strain WR. Note a - these sites
indicate the start of 60 amino acid tandem repeating units which have a
consensus sequence. The signal peptide sequence is not found in purified
35K protein recovered from the medium of cells infected with vaccinia
virus strain WR. A suggested use is to treat diseases due to abnormally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-7239208-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deduced sequence of complement 4b (C4b) binding protein Vaccinia virus WR strain; anti-complement protein; complement inactivators; complement 4b; C4b.
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Kotwal G;
                                                                                                       Control elements; gene expression; endothelial cells; megakaryocytes; rheumatoid arthritis; ischaemic injur atherosclerosis; bacterial sepsis; tumour metastases.
                                                                                                                                                                                                  R65216 standard; Protein; 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 high complement activity.
             02-MAR-1995.
19-AUG-1994; U09395.
20-AUG-1993; US-110158.
(OKLA ) UNIV OKLAHOMA STATE.
                                                                                                                                                      P-selectin
                                                                                                                                                                    04-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                                             154
                                                                                                                                                                                                                                                                                              208 HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
                                                                                                                                                                                                                                                                                                                              134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
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                                                                                                                                                                                                                                                                 SPDVINGSPISQ-KIIKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                           ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
                                                                                                                                                                                                                                                                                                                                                                                           FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                        LDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEPPISESVKCQSPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 AA;
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nce of complement 4b (C4b) binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
37; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 371; DB 1; Pred. No. 6.80e-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   below."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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              retroviral vector particle expressing complement inhibitor activity properties and complement inhibitor activity properties and complement inhibitor activity properties and complement inhibitor sequence comprises the herpesvirus Saimiri secreted complement sequence comprises the herpesvirus Saimiri secreted complement complement complement complement complement and complement and complement are the protected from inactivation upon exposure to body fluids containing complement. Also claimed are: (1) a producer cell producing the vector particles and (2) a chimeric complement are recovered from the vector particles and complement complement complement complement complement inhibitor activity. The containing a complement inhibitor activity. The containing a claimed method for transducing cells in the complement activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression control elements in the 5' flanking region of the p-selectin gene for regulating gene expression in endothelial cells and mega:karyocyte(s) Disclosure; Fig 1; 88pp; English. The sequence is that of the P-selectin gene product from endothelial cells, determined from a composite of four overlapping cDNAs: lambda GMPE1 lambda GMPE4. The P-selectin gene or its fragments may be used to inhibit P-selectin expression, thus controlling inflammatory and haemostatic processes in e.g. rheumatoid arthritis, ischaemic injury, bedreved.
                                                                                                                                                                                                                                                                                                                                       01-JUL-1997.
21-JUL-1994;
21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 95-106847/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                       N-PSDB; T84474.
                                                                                                                                                                                                                                                                                       Mason JM, Squinto WPI; 97-350243/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpesvirus Saimiri strain #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem cell
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                                                                                                                                                                                                                                                                                                                         (ALEX-) ALEXION PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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  presence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 TESG-WR-PLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 DNLGQWTAPAPVCQALQCQDLPVPN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 17.0%;
Local Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFWSKEKPKCVEISCKSPDV-INGS-PISQKI-IYKENERFQYKCNMGYEYSERGDAV-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHWSAPLPTCEAISCEPLESPVHGSMDCSPSLRAFQYDTNCSFRCAEGFMLRG-ADIVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
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830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rus secreted glycoprotein sCCPH. complement inhibitor; retroviru
                                                                                                                                                                                                                                                                                                         Squinto SP;
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  body fluid containing complement, preferably ex vivo
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 344; DB 1; Length 830; Pred. No. 5.67e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retrovirus; vector; gene therapy;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders and to develop other prods.

Disclosure; Page 37-39; 59pp; English.

Gene sequences for 3 complement regulatory proteins encoded within the genome of herpesvirus Saimiri (HYS) are disclosed, i.e. membrane complement control protein homolog (mCCPH) (Q66956), secreted complement control protein homolog (seCPH) (Q66957) and HYS-15 (Q66958). mCCPH and sCCPH share substantial homology with the human complement inhibitory proteins factor H, CD35, CD46, CD55 and C4bp, which inhibit C3 convertase activity in the complement cascade. The gene sequences and corresponding proteins (R55792-94) can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New complement regulatory proteins of Herpes virus Saimiri - are used to inhibit complement-mediated lysis in treating immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sCCPH; secreted complement control protein homolog; mCCPH; membrane complement control protein homolog; HVS-15;
156 GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1994.
12-JAN-1993; U00672.
12-JAN-1993; WO-U00672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement regulatory protein; complement inhibitory protein.
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Herpesvirus saimiri sCCPH.
                                                                                                                                                            100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9416062-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    especially for gene therapy, e.g. of hereditary or acquired blood disorders by transduction of haematopoietic stem cells. Sequence 302 AA;
                                                                                                                                                                                                                                                                       44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
                                                                                                                                                                                                       24 YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 DVING-SPISOKIIYKENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 GTHTNVK-DF-YTYLDTYTYSCNDETKLTLTGPSSKLCSETGSWYPNGETKCEFIFCKLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 74; Conser
                                                                                                                                   NLY-YGSVITYTONSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                       NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94-249210/30.
                                                                                                                                                                                                                                                                                                                                                                                            h 16.8%;
Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the complement arm of the immune system. e 302 AA;
                                                                                                                                                                                                                                                                                                                                                            Conservative
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llarity 31.9%;
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Pred. No. 1.19e-24;
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Pred. No. 1.19e-24;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 302;
                                                                                                                                                                                                                                                                                                                                              91; Indels 22;
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT Retroviral vector particle expressing complement inhibitor activity PT for transducing cells in body fluids containing complement Disclosure; Column 50-52; 32pp; English.

CC This protein sequence comprises the herpesvirus Saimiri membrane CC glycoprotein mcCPH, an inhibitor of complement inhibitor such as CCPH, and are thus protected from inactivation upon exposure to CC producer cell producing the vector particles express a complement are: (1) a CC producer cell producing the vector particle; and (2) a chimeric CC producer cell producing the vector particle; and (2) a chimeric CC retroviral envelope protein (see also W26324) with at least part CC of the N-terminal receptor-binding domain removed and replaced by CC aprotein domain having a complement inhibitor activity. The CC presence of a body fluid containing complement, preferably ex vivo, CC especially for gene therapy, e.g. of hereditary or acquired blood CC disorders by transduction of haematopoletic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΨ
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22-FEB-1995 (first entry)
                                        R55792;
                                                                 R55792 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                          196 DVING-SPISQKIIYKENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC 244
                                                                                                                                                                                                                                                                214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                        156 GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRYDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T84473
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21-JUL-1994; 278630
21-JUL-1994; US-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mason JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 8
W26319 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALEX-) ALEXION PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W26319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 31.9%; tes 74; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                      IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVING-SPISQKIIYKENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 AA;
                                                                         Protein; 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide
21. .360
/label= Mat_protein
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Pred. No. 1.19e-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New complement regulatory proteins of Herpes virus Saimiri - are provided to inhibit complement-mediated lysis in treating immune disorders and to develop other prods.

Sistemant in the develop other prods.

Sistemant regulatory proteins encoded within Gene sequences for 3 complement regulatory proteins encoded within complement control protein homolog (mcCPH) (066956), secreted complement control protein homolog (mcCPH) (066957) and HVS-15 complement control protein homolog (scCPH) (066957) and HVS-15 complement control proteins factor H, CD35, CD46, CD55 and C4bp, C066958). mcCPH and sCCPH share substantial homology with the human C complement inhibitory proteins factor H, CD35, CD46, CD55 and C4bp, CM16h inhibit C3 convertase activity in the complement cascade. The gene sequences and corresponding proteins (R55792-94) can be used to control the complement arm of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                         07-MAR-1996.
30-AUG-1995; AU0553.
30-AUG-1994; AU-007724.
(AUST-) AUSTIN RES INST.
Christiansen D, Loveland
WPI; 96-160368/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mCCPH; membrane complement control protein homolog; sCCPH; secreted complement control protein homolog; HVS-15; complement regulatory protein; complement inhibitory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9416062-A.
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12-JAN-1993; WO-U00672.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD46; recombinant protein; short consensus repeat; SCR;
regulator of complement activation; transgenic animal; plg;
Disclosure; Page 32-33; 60pp; E
A cDNA sequence (T17595) codes
                                                                                                   Increasing prodn. of recombinant proteins, the amt. of A and/or T in an A and/or T ri
                                                                                                                                                                                                                                                                                                                                                                                  WO9606937-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD46 wild-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R93939 standard; Protein; 376
                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 DVING-SPISQKIIYMENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 16.8%;
Local Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94-249210/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVFEYGVKAVYTCNEGYQLLGEINYREC -- DTDG -- - WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 ĀA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                          Loveland B, McKenzie IFC,
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Pred. No. 1.19e-24;
         English.
s for wild-type CD46 (R93939), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                     Matches
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-1996.
30-AUG-1995; AU0553.
30-AUG-1994; AU-007724.
30-AUSTIN RES INST.
(AUST-) AUSTIN RES INST.
Christiansen D. Loveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulator of complement activation. Expression of CD46 in eukaryotic host cells, e.g. COS-7 and CHO-KI, is facilitated by lowering the A+T content of the short consensus repeat regions of the CD46 gene (see T17596-99) to give products (R93940-43) useful e.g. as immunomodulators. Modified CD46 may also be expressed on the organs of transgenic animals of use for organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplantation.
                                                                                                                                                                                                                                    Claim 12; Page 36-37; 60pp; English.

CD46 subSCR3 (R93941) is the product of a cDNA construct
(R17597) obtd by splice overlap extension PCR of wild type CD46
(R17595). The A+T content of AT rich exon 5 of the CD46
(R17595). The A+T content of AT rich exon 5 of the CD46
(R17595). The A+T content of AT rich exon 5 of the CD46
(R17595). The A+T content of AT rich exon 5 of the CD46
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(R17595). The A+T content of AT rich exon 5 of the CD46
(R17595). The A+T content of AT rich exon 5 of the CD46
(R17597) obtd. Type CD46
(R17597) obtd. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD46; recombinant protein; short consensus repeat; SCR; regulator of complement activation; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD46 construct subSCR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R93941 standard; Protein; 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing prodn. of recombinant proteins, esp. CD46 - by reducing the amt. of A and/or T in an A and/or T rich region of encoding ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T17597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9606937-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 DGSDTIVCDSNSTWDPPVPKC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 -WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 81; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
33 DACEE-PPTTEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERGDA-VC-TESGW-RPLPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96-160368/16.
                                                                                                                                                                                                                    pigs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 AA;
                                                                                                                                                                                           provides organs suitable for transplantation.
377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loveland B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.5%;
                                                                                                  16.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 335; DB 1;
Pred. No. 5.29e-24;
                                                                     Score 335; DB 1;
Pred. No. 5.29e-24;
54; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milland
                                                                                                                                     Length 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animal; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 27;
                                                                                  Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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PERSULT ACCOUNTS OF THE COLOR O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y Surfaces which prevent or reduce complement activation - having surface bound homologous complement restriction factor Example 1; Fig 1A; 50pp; English.

C The present sequence is human MCP, which was used in the development of a novel surface bound to a homologous complement restriction factor (HCRF), where the surface is not a surface to which HCRF binds in vivo. The surface can be used in medical caparatus (e.g. extra-corporeal circulation systems, tubing, valves, membranes, pumps, oxygenators, catheters, cannulas, fluid reservoirs or prostheses), medical dressings, surgical equipment, caparatus (e.g. kits for determining whether a patient has can abnormality which prevents the complement system from working normally or from being properly regulated) and purification can be used to reduce or prevent activation of complement, and to sequence morbidity due to complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1996;
22-MAR-1996;
28-MAR-1996;
116 -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T90306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watkins NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; MCP; surface; homologous complement restriction factor; HCRF; medical apparatus; medical dressing; surgical equipment; diagnostic kit; prevention; purification device; reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMUT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W27484 standard; Protein; 377 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2-MAR-1997;
                                                                                                                                                              58
                                                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                                                                                                                33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 81; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149
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                                                                  IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 205
                                                                                                                                        PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                                       D-DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVA 148
                                                                                                                                                                                                                                                                                 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97-489571/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGDA-VC-TESGW-RPLPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGSDTIVCDSNSTWDPPVPKC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB-022694.
GB-006073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB-006516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G00684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.5%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 335; DB 1;
Pred. No. 5.29e-24;
54; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant mammalian membrane co-factor protein - for treating diseases with altered complement activity e.g. inflammatory and auto-immune conditions
Disclosure; fig 1; 38pp; English.
This human isoform of a membrane cofactor protein (MCP) is useful in a pharmaceutical compsn. for the treatment of inflammatory and autoimmune diseases mediated by excess or misdirection of complement activity e.g. rheumatoid arthritis or multiple sclerosis. Protection against tissue injury caused by e.g. myocardial infarction or stroke may also be provided. Antibodies raised farction or stroke may also be provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against this MCP can be used in autoimmune disease diagnosis to predict the probability of recurrent miscarriages by testing for MCP levels in the placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also Q10865-66 and R10927.
170 EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYS 226
                                                                                                                    116 -WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD 169
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19-APR-1990; US-510709.
(UNIW ) UNIV OF WASHINGTON.
                                                      206 STIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YL 262
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20-JUL-1990;
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                                                                                                                                                                                                                                              58 PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                             33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 335; DB 1;
Pred. No. 5.29e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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227

ERGDA-VC-TESGW-RPLPSC 244 DGSDTIVCDSNSTWDPPVPKC

283

Human CD46

15-APR-1996

(first

entry)

R86316 standard; Protein; 384

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Disclosure; Page 66-68; 85pp; English.

A terminal complement inhibitor protein (CIP), is used in the romatruction of chimeric cDNA coding for transmembrane terminal CIP, pref. comprising amino acids 1-77 of CD59 fused to amino acids 270-350 (the transmembrane domain) of CD46 (R86316). Such chimeric cDNA is incorporated into a retrovirus vector and used in the breeding of transgenic animals as a means of producing transgenic organs that are protected against human complement
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          09-NOV-1998 (first entry)
09-NOV-1998 (first entry)
rsMCP protein SEQ ID NO:25 from WO9829453 Claim 14.
Drug; cell membrane-directed drug; phospholipid; lipid bilayer;
Drug; cell membrane-directed drug; inflammation; immunological dis
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                                                                                                                                                                           W69523 standard; peptide; W69523;
   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 205
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ilarity 31.0%;
Conservative
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                                                                                                                                                                                                               279 AA
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Pred. No. 5.29e-24;
54; Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT blood coagulation, inflammatory and immunological disorders
PS Claim 14; Page 81-83; 117pp; Japanese.
CC The present invention describes drug compositions which contain as
CC an active component a peptide which has specific affinity to particular
CC especially to phospholipids which constitute a lipid bilayer of cellular
CC especially to phospholipids which constitute a lipid bilayer of cellular
CC expecially to phospholipids which constitute a lipid bilayer of cellular
CC which are abnormal (e.g. through injury, denaturation or activation). In
CC which are abnormal (e.g. through injury, denaturation or activation). In
CC which are structure of formula (1): (Al)a-(A2)b-(A3)c, where (A1) is one of
CC and a structure of formula (1): (A1)a-(A2)b-(A3)c, where (A1) is one of
CC two specific sequences (see W69516 and W69519), (A2) and (A3) are
CC (C (EXPLAIRIHPOSWYHGIALR, LRYLRIHPOSWYHGIALR, (see W69511) or MEYLGCEAQNLY (see
CC (EXPLAIRIHPOSWYHGIALR, LAVLRIHPOSWYHGIALR) and c = 0-5. Preferred are the formulae
CC (A2-A2-A3 or A2-A2). The sequence is linked to a peptide such as a
CC (A2-A2-A3 or A2-A2). The sequence is linked to a peptide such as a
CC (A2-A2-A3 or A2-A2). The sequence is linked to a peptide such as a
CC (A2-A2-A3 or A2-A2). The drugs are used for the treatment and prevention of
CC diseases involving blood coagulation, inflammatory and immunological
CC discorders. The present sequence represents a peptide from the present
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Best Local Similarity
Thes 85; Conser
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05-JAN-1998; J00002.
27-DEC-1996; JP-359053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drugs containing peptide(s) with specific affinity to phospholipid(s) - such as phosphatidyl serine, for treatment of blood coagulation, inflammatory and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hasegawa T, Kuriyama S; WPI; 98-388051/33. N-PSDB; V40047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9829453-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                             117
                                                                                           172
                                                                                                                                      174
    229
                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                    58
                                                                                                                                                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                               1 CEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSD-
                                                                                                                               IYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YLDG
                                                                                                                                                                                                                                                                                                               DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIW 116
                                                                                                                                                                                                                                                                                                                                                              CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALNPL 59
                                                                                         MHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYSER
                                                                                                                                                                                  TNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGDEE
                                                                                                                                                                                                                          SGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGEST
                                                                                                                                                                                                                                                                          RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG-W
    GDA-VC-TESGW-RPLPSCEEKSCDNPYIPN-GDYS
                                            SDTIVCDSNSTWDPPVPKCL-KGPRPTYKPPVSNYP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 333; DB 1;
Pred. No. 8.68e-24;
57; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 105;
         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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29			
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

tun on: Thu Jun 8 21:41:21 2000; MasPar time 16.86 Seconds
741.518 Million cell updates/sec

Tabular output not generated.

Title: >US-09-316-163-10
Description: (1-265) from US09316163.pep
Perfect Score: 2029

Sequence: 1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK 265

Scoring table: PAM 150
Gap 11

earched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Lighting figst 45 summaries

Database: Listing if

Statistics:

1:pird 2:pir2 3:pir3 4:pir4

Mean 43.012; Variance 68.118; scale 0.631

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 2029	Query Match	,	DB	ID NBHUHS	Description complement factor H p	
2 ⊢	2029	100.0	1231	- +	NBHUH	factor	0.00e+00
ω	1439	70.9	1234	L	NBMSH	nt factor H	0.00e+00
4	952	46.9	669	N	865551		9.39e-21
տ	587	28.9	1053	N	S46199	probable complement r	3.83e-11b
σ,	406	20.0	597	ш	S53711	C4BP alpha chain prec	
7	388	19.1	263	ب	WMVZSP	apolipoprotein H homo	
ω.	382	18.8	597	1	NBHUC4	C4b-binding protein a	8.650-6
9	371	18.3	345	Н	NBMS	7	
10	371	18.3	558	N	S57953		4.20e-62
11	357	17.6	263	Н	C36838	complement control pr	1.056-5
12	353	17.4	560	N	T16833	hypothetical protein	9.926-5
13	344	17.0	830	N	A30359	p-selectin precursor	1.49e-5
14	341	16.8	302	ب	WMBELE	secretory complement	1 ~
15	341	16.8	360	Н	WMBE2E	membrane-bound comple	ı ~
16	341	16.8	469	ب	NBMSC4	9	7.888-55
17	341	16.8	768	2	153821	1	• :
18	338	16.7	349	N	G02913	sperm CD46 - human (I	
19	338	16.7	369	N	I57998	membrane cofactor pro	4.160
20	338	16.7	610	ب	146001	C4b-binding protein a	4.15e-54
21	339	16.7	768	N	A42755	P-selectin precursor	٠,
22	334	16.5	345	ب	NBBO	apolipoprotein H prec	3.828-5
23	335	16.5	377	2	I54479	membrane cofactor pro	۲.

ALIGNMENTS

#cross-references MIID: #accession A27877 ##molecule_type_mRNA ##residues an a ##note	#authors #journal #title	tatus olecule_ esidues ote	#authors #journal #title #cross-referen #accession	#accession S03013 #accession S03013 ##molecule_type mRNA ##residues	RESULT 1 ENTRY TITLE ALTERNATE_NAMES CORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title #title
#cross-references MUID:87054207 #accession A27877 #accession A27877 #accession A27877 #imolecule_type mRNA	Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P. Eur. J. Immunol. (1986) 16:1351-1355 Human complement factor H: isolation of cDNA clones and partial cDNA sequence of the 38-kDa tryptic fragment containing the binding site for C3b.	not compared with conceptual translation type mRNA 1-33,434-449 ##label EST only portions of this 1.8 kilobase mRNA were sequenced	REFINE AD0230 authors Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. ijournal Eur. J. Immunol. (1991) 21:799-802 title Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts. icross-references MUID:91184292 accession B60238	#cross-references MUID:88134059 #accession S03013 ##molecule_type mRNA ##residues 1-449 ##label RIP ##cross-references EMBL:XO7523; EMBL:Y00716; NID:932492; ##cross-references EMBL:XAA30403.1; PID:9758073 ##note mature protein was confirmed by protein sequencing ##note 402-Tyr was also found	NBHUHS #type complete complement factor H precursor, short splice form - human complement factor H-related protein; complement protein H #formal_name Homo sapiens #common_name man 31-Dec-1993 #sequence_revision 23-reb-1996 #text_change 22-Jun-1999 \$303013; B60238; A27877; A61103; A26505; S10479 \$00254 Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B. Biochem. J. (1988) 249:593-602 The complete amino acid sequence of human complement factor the complete amino acid sequence of human complement factor

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CLASSIFICATION
                                                                                                              FEATURE
                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                     FUNCTION
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    21-80
                                                                  19-449
                                                                                                                                                                                                                            #pathway
                                                                                                                                                                                                                                                                                                                          #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #gene GDB:HF1; HF ##CTOSS-references GDB:120041; OMIM:134370 #map_position 1q32-1q32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal
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**Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-3634

**title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title Purification and structural studies on the complement-system control protein beta-1-H (factor H).
#cross-references_MUID:83048213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GDB:129095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 226-401,'Y',403-449 ##label KRI
##cross-references GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473
Factor H has also been found bound to cell membranes in an unknown manner. However, it has at least one cell attachment site motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
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##molecule_type mRNA
##moridines 27-76 ##label SC2
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##mesidues 19-20,'Q',22-29,'V',31-33,'Q',35 ##label SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in liver. See also PIR:NBHUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in repeat 4.
                                                                                                                                                                                                      a cofactor in the inactivation of C3b by serine proteinase also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
                                                                                                                                    alternative splicing; complement alternate pathway;
                                                                                                                                                                                   #superfamily complement factor H; complement factor H repeat
                                                                                                                                                                                                                                                                                                                                                                                              the correspondence between the two loci and the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDB:HF2; HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kristensen, T.; Wetsel, R.A.; Tack, B.F.
J. Immunol. (1986) 136:3407-3411
Structural analysis of human complement protein H: homology with C4b binding protein, beta(2)-glycoprotein I, and the Ba fragment of B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S10479
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Biochem. J. (1982) 205:285-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation; NMR structure determination, residues 264-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A61103
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Eur. J. Immunol. (1987) 17:1485-1489
Human complement factor H: expression of an additional truncated gene product of 43 kDa in human liver.
                                                                                                                             glycoprotein; plasma
                                                                                                                                                                                                                                                                                                                                                               several allelic forms
                                                                                                                                                                                                                                                                                                                                                                                     indicated
                   #domain signal sequence #status predicted #label SIG\
#product complement factor H, short splice form #status
experimental #label MAT\
#domain complement factor H repeat homology #label FH01\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this is a partial sequence of an alternatively spliced 1.8 kilobase mRNA that is translated to yield a 43 K form related to factor H
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                                                                                                                                                                                                                                                                                                                                                                           is unclear; factor H has been reported to have
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                      ##status
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#cross-references MUID:91184292
#accession A60238
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178-205,210-251,
237-262,267-309,
294-320,325-374,
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357-385,389-431,
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                                                                                                                                                                                                                                            ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LPSCEEKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 LPSCEEKSCDNPYIPNGDYSPLRIK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 KCOKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
Similarity 100.0%;
                                                                                Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived,
from alternatively spliced transcripts.
                                                                                                                                                                                                                                                                                                                                                                                              S00254
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete amino acid sequence of human complement factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B Biochem. J. (1988) 249:593-602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBHUH #type complete complement factor H precursor, long splice form - human formal_name Homo sapiens #common_name man 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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             not compared with conceptual translation
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complement factor H repeat homology #label complement factor H repeat homology #label complement factor H repeat homology #label complement factor H repeat homology #label
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Pred. No. 0.00e+00;
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#title Partial characterization of human complement factor H by protein and cDNA sequencing: homology with other complement #cross-references MUID:86188123
#accession A61565
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#title Sequence analysis of a cDNA clone encoding the C-terminal end of human complement factor H.
#cross-references MUID:88025472
#accession A54726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Sim, R.B.; Discipio, R.G.
#journal Biochem. J. (1982) 205:285-293
#title Purification and structural studies on the complement-system
control protein beta-1-H (factor H).
#cross-references_MUID:83048213
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pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-3636

Biochemistry (1992) 31:3626-3636

Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.

#cross-references MUID:92232649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title Three-dimensional structure of a complement control protein module in solution.
#cross-references MUID:91278097
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                                                                                                                                                                                                                                                                                                                   J. Immunol. (1991) 146:3190-3196 (Cloning of the 1.4-kb mRNA species of human complement factor H reveals a novel member of the short consensus repeat family related to the carboxy terminal of the classical 150-kDa molecule.
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                          Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon, D.L.; Burns, G.F.
Biochim. Biophys. Acta (1996) 1289:305-311
Factor H co-purifies with thrombospondin isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation; NMR structure determination, residues 927-985
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#map_position 1q32-1q32
#note
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#accession S66298
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325-385
389-442
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781-803,811-853,
839-864,870-915,
901-926,931-973,
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691-744
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597-623,630-673,
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##residues 411-419;574-578,580-582 ##label CAR
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#authors
                                                                                                                                                        #authors Natsuume-Gakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y.
#journal J. Immunol. (1990) 144:358-362
#title Demonstration of an unusual allelic variation of mouse factor
#toross-references MUD:90111033
#cross-references MUD:90111033
                                                                                                                                                                                                                                                                                                                                                                     *authors Kristensen, T.; Tack, B.F.

*journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967

*title Murine protein H is comprised of 20 repeating units, 61 amino *cross-references MUD:86233353

*cross-references MUD:86233353

*accession**
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1077-1102,
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1018-1043,
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                                            ##residues 1-18 ##label RES ##cross-references GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729
                                                                                                ##molecule_type mRNA
                                                                                                                         ##status
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##residues 1-1234 ##label KRI
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Similarity 100.0%;
265; Conservative
        Munoz-Canoves, P.; Tack, B.F.; Vik, D.P
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536-564,569-610,
597-622,629-672,
658-683,690-732,
718-743,752-791,
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178-205,210-251,

237-262,267-309,

294-320,325-374,

357-385,389-431,

416-442,448-494,
                                                                                            1053-1096,
1082-1107,
1114-1157,
1114-1168,
                                   676,721,773,801,
1030,1061,1225
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1053-1107
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1172-1233
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##cross references GB.J02891; NID.g193805; PIDN:AAA37795.1; PID:g553926
NT Two codominant alleles of factor H are present in mice.
NT Factor H functions as a cofactor in the inactivation of C3b by
serine proteinase I and also increases the rate of dissociation
of the C3bbb complex (C3 convertase) and the (C3b)nBb complex (C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
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   predicted #mu
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Analysis of complement factor H mRNA expression:
Dexamethasone and IFN-gamma increase the level of H in L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
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                                                                                                                        140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##status
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Local Similarity 67.0%;
    187 RP 188
                                      200 GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDY 259
                                                                                                                                                                  67
                                                                                                                                                                                                      08
                                                                                                                                                                                                                                           7 LAEGNOFEYGAKVVYTCDEGYOMYGEMNFRECDTNGWINDIPICEVVKCLPVTEPENGKI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICRKKPCGHPGDTPFGSFRLAVGSQFEFGAKVVYTCDDGYQLLGEIDYRECGADGWINDI 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNEKPRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGDAVCTGSGWSS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLCEVVKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLW 198
                                                                               GQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIPNGVY 186
                                                                                                                                                             FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                                                           LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                  h 46.9%;
Similarity 64.3%;
117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soames, C.J.; Day, A.J.; Sim, R.B.
Blochem. J. (1996) 315:523-531
Prediction from sequence comparisons of residues of factor H
involved in the interaction with complement component C3b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor H - bovine (fragment)
#formal_name Bos primigenius taurus #common_name cattle
#formal_name Bos primigenius taurus #common_name cattle
19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #superfamily complement factor H; complement factor H repeat
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                                                                                                                                                                                                                                                                                      Score 952; DB 2; L
Pred. No. 9.39e-211;
29; Mismatches 36:
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6:
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#journal Biochem. J. (1994) 301:391-397
#title Cloning and characterization of a cDNA representing a protein from barred sand bass (Parablax neblifer).
#cross-references MUID:94318039
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935-989
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569-624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:L21703; NID:g639894; PID:g639895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type protein
##residues 526-532,'X',534-537;809-817,'X',819-826 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                      257
                                                                                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                        141 SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN
                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQV 161
                                                                                                                                                                                                          279 TRYEP 283
                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 EASYPGGROVRVGCNVGY-S-GFFKLVCVEGKWETRGA--KCQPRSCGHPGDAQFADFHL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                 TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV
                                                                                                                                                                    GDYSP 261
                                                                                                                                                                                                                                            GSPISQKIIYKENERFQYKCNMGYEYSERGDA-V--CTESGWRPLPSCEEKSCDNPYIPN
                                                                                                                                                                                                                                                                                GNVPGAIREYKENDVLHYECDRAFKHIDRPSTCIKQGIKAEWSPTPLCESIKCRLTIMDG 278
                                                                                                                                                                                                                                                                                                                                                           IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%;
Similarity 37.1%;
91; Conservation
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                   10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                       #formal
                                                                         C4BP alpha chain precursor - rabbit
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                                                       _name Oryctolagus cuniculus #common_name domestic
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                                                                                           #type complete
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Pred. No. 3.83e-116;
41; Mismatches 101;
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factor H repeat
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                                                                                                                                                                                                          #authors Kotwal, G.J.; Moss, B.
#journal Nature (1988) 335:176-178
#title Vaccinia virus encodes a secretory polypeptide structurally
#cross-references MUD:88318974
#cross-references MUD:88318974
                               #authors
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                                                                            ##experimental_source strain WR
                                                                                                        ##residues 1-263 ##label KOT
##cross-references GB:X13166; NID
                                                                                                                                    ##residues
                                                                                                                                                     ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 NSCLGLPNVPHA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 IINGK-HNGGNE-DIH-TYGSSVTYSCNPRFSLLGEASISCTVKNKTVGVWSPSPPVCKE 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEVKT-D-FSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVEWSDPLPKCEIVKCEPPPN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDQTYPEGTQAIYKCREGYRSLG-NVIMYCR-KGEWVALNPLKKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENEYQTGTILKYTCRPGYTRNGLNPILTCKPRGLW-SYDTF--CVKKRCRNPGDLPNGQ 122
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Similarity 32.9%;
                      Goebel, S.J.; Johnson, G.P.; Perkus,
                                                           A4250:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WMVZSP #type complete
apolipoprotein H homolog precursor - vaccinia virus
35K secretory protein; C3L protein; virokine
#formal_name vaccinia virus
                                                                                                                                                                                          A31005
                                                                                                                                                                                                                                                                                                                                                                           A31005; B42504
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Biochim. Biophys. Acta (1995) 1261:285-289
cDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein
modules which bind C4b.
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                                                                                                  NID: g60690; PIDN: CAA31564.1;
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                      ĭ.E.,
                   Davis, S.W.;
                                                                                               PID:g60691
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206-261
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Lintin, S.J.; Lewin, A.R.; Reid, K.B.M
                                    S02372
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Query Match 19.1%;
Best Local Similarity 34.2%;
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##molecule_type mRNA
##residues 1-597 ##label MA1
##cross-references GB:M31452; NID:g1905
##note the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 ISNGR--HNGYE-DF-YIDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
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##cross-references GB:M35027; NID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ANANYNIGDTIEYLCLPGYRKOKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                          NBHUC4 *type complete C4b-binding protein alpha chain precursor - human C4BP; proline-rich protein *formal_name Homo sapiens *common_name man 13-Aug-1986 *sequence_revision 30-Jun-1993 *text_change
                                                                                                                                                                        Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y. Biochem. Biophys. Res. Commun. (1989) 165:138-144
Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein.
                                                                                                                                                                                                                                                                                                                                                             A33568; S02372; A90326; A24182; A93134; S29492; A31785;
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The complete DNA sequence of vaccinia virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily herpesvirus complement control complement factor H repeat homology duplication; extracellular protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation; possible protein-coding frames neither amino acid nor nucleotide sequence is given
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#product C4b-binding protein homolog #status predicted
#label MAT\
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Pred. No. 2.94e-66;
37; Mismatches 96
                                         NID:g190501;
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      the codon GGA for residue 492 as
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#title Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of
the C4bp cDNA sequence.
#cross-references MUID:88242821
#accession S02372
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                                               C4b-binding protein. #cross-references MUID:89034204
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##cross-references EMBL:X07853
##note although the sequence determined extends to residue 9
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##molecule_type protein
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##molecule_type protein
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##residues 49-81 ##label CH1
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Chung, L.P.; Bentley, D.R.; Reid, K.B.M.
Biochem. J. (1985) 230:133-141
Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.
                                                                                                                                                                                                                                                                                                                           Hessing, M.; Kanters, D.; Takeya, H.; van't Veer, C.;
Hackeng, T.M.; Iwanaga, S.; Bouma, B.N.
FEBS Lett. (1993) 317:228-232
The region Ser(333)-Arg(356) of the alpha-chain of human
C4b-binding protein is involved in the binding of
complement C4b.
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Mol. Immunol. (1985) 22:427-435
Amino acid sequence studies of human C4b-binding protein:
N-terminal sequence analysis and alignment of the fragments
produced by limited proteolysis with chymotrypsin and the
peptides produced by cyanogen bromide treatment.
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FEBS Lett. (1986) 204:77-81
Studies on the structure of the human C4b-binding protein
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                                                                                            Suzuki, K.; Nishioka, J.
J. Biol. Chem. (1988) 263:17034-17039
Binding Site for vitamin K-dependent protein S on complement
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                                                                                                                                                                                                  381-404 ##label HES
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1-597 ##label ASO

##cross-references GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500

##cross-references GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g1905000

##cross-references GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500

##cross-references GB.M62486; NID:g190498; PIDN:AAA3660.1; PID:g190500

##cross-references GB.M62486; NID:g190498; PIDN:AAA3660.1; PID:g190500

##cross-references GB.M62486; NID:g190498; PIDN:AAA3660.1; PID:g190500

##cross-references GB.M62486; NID:g190500

##cross-references GB.M62486; NID
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#title
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Best Local
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#title Genomic organization of the alpha chain of the human
C4b-binding protein gene.
#cross-references_MUID:91113199
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381-404
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175-234
239-294
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#map_position 1q32-1q32
#introns 48/1; 110/1; 143/2; 172/1; 236/1
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                                                                     67 TETREKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 123
                                                                                                                                                   / Match 18.8%;
Local Similarity 31.5%;
nes 79; Conservative
20 SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
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    ligand binding
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#domain complement factor H repeat homology #label FH7\
#domain complement factor H repeat homology #label FH8\
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                                                                                                                                                                                                                                                                                                                    #molecular-weight 67033 #checksum 6374
                                                                                                                                                   Score 382; DB 1;
Pred. No. 8.65e-65;
52; Mismatches 98
                                                                                                                                                                98;
                                                                                                                                                                                                                                      Length 597,
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23-66,51-79,84-124,
110-137,142-188,
174-200,205-248,
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23-79
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Whitehead, A.S.
#journal Biochem. Biophys. Res. Commun. (1994) 200:1521-1528
#title Characterization, expression and evolution of mouse
beta2-glycoprotein I (apolipoprotein H).
#cross-references MUID:94242017
                                                                                                                                                                                                                                                                                                                                                                                                                 #gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #cross-references MUID:92372000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GB:S70439; NID:g546780; PIDN:AAB30789.1; PID:g546781 ##experimental_source liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-252,'A',254-277,'N',279-345 ##label NON ##cross-references GB:D10056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCINLPDIPHA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCDN-PYIPNG 257
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                                                                                                                                                                                                                                                                                                                                                #superfamily apolipoprotein H; complement factor H repeat
                                                                                                                                                                                                                                                                                                            chylomicron; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                          B2gp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.; Natsuume-Sakai, S.
Genomics (1992) 13:1082-1087
Molecular cloning of mouse beta-2-glycoprotein I and mapping
of the gene to chromosome 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NBMS #type complete
apolipoprotein H precursor - mouse
50K serum glycoprotein; activated protein C-binding protein;
beta-2-glycoprotein I
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A43286
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
28_May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nonaka, M.; Matsuda, Y.; Shiroishi,
                                                                                                                                                                                                                                                                                                                                   homology
                                                                                                                                                                                                                                                                                   lipid binding; monomer;
                                                                              #domain signal sequence #status predicted #label SIG\
#product apolipoprotein H #status predicted #label MAT\
#domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH4\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the authors translated the codon ACT for residue 253 as Ala and ATG for residue 278 as Asn sequence extracted from NCBI backbone (NCBIN:111791, NCBIP:111794) and corrected to correspond with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide translation
                                                                                                                                                                                                                                                                                glycoprotein;
plasma; VLDL
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                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                             15-72
77-134
139-199
204-258
263-324
328-386
390-443
447-501
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Best Local Similarity 29.4%;
Matches 74; Conservative
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300-307,325-345
105,117,162,183,
193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:250051; NID:g899379; PIDN:CAA90391.1;
PID:g899380
FICATION #superfamily C4b-binding protein alpha chain; complement
                                                               43 YNCRPGYSRASSSQSLYCKPLGKW-QIN-IA-CVKKSCRNPGDLQNGKVEVKT-D-FLFG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 NG--S-PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI 254
32 YKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 KATVLYQGMRVK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI 198
                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 SYDPGEQIVYSCKPGYVSRGGMRRFTCPLTGMW-PINTLR-CVPRVCPFAGILENGIVRY 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGYVNYPAKPVLLYKDKATFG--CHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVK 269
                                                                                                                                     18.3%;
Similarity 30.5%;
73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillarp, A.; Thern, A.; Dahlback, B. submitted to the EMBL Data Library, July 1995 Molecular cloning of rat C4b-binding protein alpha- and beta-chains: structural and functional relationships a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $57953  #type complete C4BP protein alpha chain precursor - rat  #formal_name Rattus norvegicus #common_name Norway rat  13-Jan-1996  #sequence_revision 01-Mar-1996  #text_change
                                                                                                                                                                                                                                                                              #length 558
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                                                                                                                              Score 371; DB 2; Length 558; Pred. No. 4.20e-62; 57; Mismatches 87; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 371; DB 1; Length 345; Pred. No. 4.20e-62; 49; Mismatches 110; Indels
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FH2/
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148-201
206-261
                                           #accession
                                                                                      #submission
                                                                 #description
                                                                                                            #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
##status preliminary; translated
##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                 207 PHPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSSSSTCSPGNTWQPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                               154 IS-NGR--HNGYN-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-263 ##label BLI
##cross-references GB:X69198; NID:g456758; PIDN:CAA48953.1; PID:g297195
FICATION #superfamily herpesvirus complement control protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 PISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRPLPSCEEKSC-DNPYIPNG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 INSGFKHTYKYKDSVRFVCQKGFVLRGSGVIHCEADGSWSPVPVCELNSCTDIPDIPNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 PDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVEISCKSPDVINGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.6%;
Local Similarity 33.6%;
nes 79; Conservation
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                                                                                                                                                                                                                                                                                                                            KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                          APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTLIGGNVFEYGVKAVYTCNEGYQLLGEIN-Y-RECDTDG--WINDIPICEVVKC-LPVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEF-FTYRSSVTYKCDPDFTLLGNASITCTVVNKTVGVWSPSPPTCERIICPWPKVLHGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKAVYTCNEGYQLLGE-INYRECDTDG--WINDIPICEVVKC-LPVTAPENGKIVSSAME 145
                                                    submitted to the EMBL Data Library, April 1996 The sequence of C. elegans cosmid T07H6.
                                                                                                                                                                           T16833 #type complete
hypothetical protein T07H6.5 - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
20._Sep-1999_ *sequence_revision 20-Sep-1999 #text_change
                                           T16833
                                                                                                        Geisel, C.
                                                                                                                                Z1858
                                                                                                                                                 T1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to GenBank, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blinov, V.M.
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10-Sep-1999 #sequence_revi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement control protein homolog - variola virus (strain
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#domain complement factor H repeat homology #label FH2'
#domain complement factor H repeat homology #label FH3'
#domain complement factor H repeat homology #label FH3'
#domain complement factor H repeat homology #label FH4
gth 263 #molecular-weight 28789 #checksum 8771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 357; DB 1; Length 263; Pred. No. 1.06e-58; 38; Mismatches 95; Indels
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                 from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 263;
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#map_position 1q22-1q25
CLASSIFICATION #superfam
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REFERENCE
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                                      448-505
510-567
572-629
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262-319
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                                                                                                             386-443
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#title
                        642-699
                                                                                                                                     324-381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #introns
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                                                                                                                                                                                                                                                                                                                                                                                                     ene GDB:SELP; GRMP ##CTOSS-references GDB:120018; OMIM:173610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-830 ##label JOH
##cross-references GB:M25322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 EEMHCSDDGFWSKEKPKCVEISCKS-PDVINGSPISQKIIYKENERFQYKCNMGYEYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 CSSNGEWINEPANCKATECSRPSSPLHGKVVGSSL-T---YQ-S-VVTYSCDHGYRLVGQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AQWFGPD-LR-CKARACPDPGDIENG----LREGDTFEYPHHVKYSCNPGFLLVGSTS-RQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 GDAVCTESG-WR-PLPSCEEKSCDNPYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 SKAKCMEDGQWSAPIPRCLA-SCRVPHIQNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNGYIEGSETSFGAVAVFRCLETMTHE-GA-
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Similarity 32.2%;
68; Conservative
                                                                                                                                                                                                                                                                                                                                                         #superfamily complement factor H repeat homology;
                                                                                                                                                                                                                                                                                                             cell adhesion; glycoprotein; phosphohistidine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A30359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnston, G.I.; Cook, R.G.; McEver, R.P. Cell (1989) 56:1033-1044 Cloning of GMP-140, a granule membrane protein of platelets and endothelium: sequence similarity to proteins involved
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P-selectin precursor - human
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#length 560
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                                                                                                                                                                                                                                                                                     phosphoprotein; surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                           homology
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#domain complement factor H repeat homology #label FH01\
#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH07\
#domain complement factor H repeat homology #label FH08\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parts of this sequence, including the amino end of the mature protein, were confirmed by protein sequencing
                                                                                                                                                                                           #domain signal sequence #status predicted #label SIG\
#product P-selectin #status experimental #label MAT\
#domain EGF homology #label EGF\
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Pred. No. 9.92e-58;
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Best Local
Best Local Similarity 31.9%;
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716,723,741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Albrecht, J.C.; Fleckenstein, B.
#journal J. Virol. (1992) 66:3937-3940
#title New member of the multigene family of complement control
#cross-references MUID:92260674
                                                                                                                                        36,39,46,72,155
                                                                                                                                                                                  147-205
                                                                                                                                                                                                            84-142
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                                                                                                                                                               210-264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 TESG-WR-PLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 DNLGQWTAPAPVCQALQCQDLPVPN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-302 ##label ALB Tresidues 1-302 ##label ALB Tresidues 1-302 ##label ALB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 17.0%;
Local Similarity 26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFWSKEKPKCVEISCKSPDV-INGS-PISQKI-IYKENERFQYKCNMGYEYSERGDAV-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length
                                                                                                                                                                                                                                                                                                                                                                  #superfamily herpesvirus complement control protein;
complement factor H repeat homology
alternative splicing; duplication; extracellular protein;
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#domain transmembrane #status predicted #label TMN\
#domain intracellular #status predicted #label CYT\
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                                                                                                                                                          #domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
                                                                                                                                        #binding_site carbohydrate (Asn) (covalent) #status
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#status predicted #label SCC\
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                                                                                             #molecular-weight 33392 #checksum 5963
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Pred. No. 1.49e-55;
                              Score 341; DB 1;
Pred. No. 7.88e-55;
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84-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPRCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL:X60283; NID:g60315; PIDN:CAA42823.1; PID:g60317
[FICATION #superfamily herpesvirus complement control protein; complement factor H repeat homology
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214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                               139 IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP 195
                                                                                         156 GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP 213
                                                                                                                                                                                       100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                     84 NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WINDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                 24 YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG
                                                                                                                                                                                                                                                                                44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
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New member of the multigene family of complement control proteins in herpesvirus saimiri.
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30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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homolog *status predicted *label SCC\
*domain complement factor H repeat homology *label FH1\
*domain complement factor H repeat homology *label FH2\
*domain complement factor H repeat homology *label FH3\
*domain complement factor H repeat homology *label FH4\
*domain transmembrane *status predicted *label TMN\
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Qy 196 DVING-SPISQKIIYKENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC 244

Search completed: Thu Jun 8 21:41:41 2000 Job time : 20 secs.

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Scoring table: Sequence: Description: Perfect Score: PAM 150 Gap 11

Post-processing: Minimum Match 08 Lightng first 45 summaries Searched: 83857 segs, 30454973 residues

Database: wiss-prot38
1:9wissprot

Statistics: Mean 43.808; Variance 61.409; scale 0.713

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23 23 24 34 35 44 36 46 47 47 47 47 47 47 47 47 47 47 47 47 47	Result
2029 1439 382 382 371 371 371 341 341 341 333 338 338 331 317 317 317 310 310 306	Score
100.0 70.9 19.1 18.8 18.3 17.0 17.0 16.8 16.8 16.8 16.2 16.5 16.5 16.5 15.6 16.5 15.6 16.7	% Query Match
1234 1234 1234 259 345 59 345 558 610 610 768 768 768 768 768 768 768 768 768 768	Length
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J. Mol. Biol. 232:266-284(1993).

-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION OF C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALITERNATIVE COMPLEMENT FATHWAY.

-i- SIMILARITY: CONVAINS 20 SUSHI (SCR) REPEATS.

-i- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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J. Mol. Biol. 219:717-725(1991).
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"Analysis of complement factor H mRNA expression: dexamethasone IFN-gamma increase the level of H in L cells.";
Biochemistry 28:9891-9897(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 90148935.
Munoz-Canoves P., Tack B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Murine protein H is comprised in length.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                  "Demonstration of an unusual allelic variation of mouse factor H by the complete cDNA sequence of the H.2 allotype.";

J. Immunol. 144:358-362(1990).

J. Immunol. 104:358-362(1990).

AS A COFACTOR IN THE INACTIVATION OF THE FUNCTION: FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF THE C3BB FACTOR I, AND ALSO INCREASES THE RATE OF DISSOCIATION OF THE C3BB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEXENT PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                      Moriwaki K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-18 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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5, Last annotation update)
precursor (protein Beta-1-H).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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EMBL; J02891; I
EMBL; M31979; I
PIR; A26154; NI
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MGD; MGI:88385; CFH.
PFAM; PF00084; sushi;
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; AAA37762.1;
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STRAIN=COPENHAGEN;
           COMPLETE GENOME
                                "The complete DNA sequence of vaccinia Virology 179:247-266(1990).
                                                                    Goebel
                                                                           STRAIN-COPENHAGEN;
MEDLINE; 91021027.
                                                                                                                   Kotwal G.J., Moss B.; "Analysis of a large cluster of nonessential genes deleted from vaccinia virus terminal transposition mutant."; Virology 167:524-537(1988).
                                                                                                                                                                                                                                                           STRAIN-WR; MEDLINE; 8
                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)
                                                                                                                                                                                                                                                                                                                                                                                                            VCP_VACCV
P10998;
                                                        Paoletti E.;
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                               STRAIN-WR;
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CARBOHYD
                                                                                                                                                                    MEDLINE; 89073756.
                                                                                                                                                                                                              Kotwal G.J., Moss B.;
"Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";
Nature 335:176-178(1988).
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                         Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                     Vaccinia virus
Viruses; dsDNA
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                                                              S.J., Johnson G.P., Perkus M.E., Davis S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Pred. No. 0.00e+
39; Mismatches
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W; C5AC02F341B957F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   263 AA.
                                                                                                                                                                                                                                                                                                                 Poxviridae;
                                         virus.";
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                                                                                                                                                                                                                                                                                                                Chordopoxvirinae;
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                                                            Winslow
                                                              J.P.,
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                                                                                                                                                                                                                                                                                                                                    REPEA
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
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PDB; 1VVC; 03-DEC-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13166; CAA31564.1; -. EMBL; M22812; AAA69605.1; -. EMBL; M35027; AAA47997.1; -.
154 ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "NMR studies of a viral protein that mimics the regulators of complement activation.";

J. Mol. Biol. 272:253-265(1997).

-:- FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Vaccinia virus complement-control protein prevents antibody-dependent complement-enhanced neutralization and contributes to virulence.",
Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barlow P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiles A.P., Shaw G., Bright J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goebel S.J., Johnson G.P., Perkus M.E.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                           78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WTNDIPICEVVKCLPVTA
                                                             97
                                                                               20 SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT
                                                                                                        40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isaacs S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 179:517-563(1990).
                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.
SIMILARTY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).
SIMILARTY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                   LDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPS 153
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat;
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                                                                                                                                         Conservative
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                                                                                                                                                    19.1%;
34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure.
                                                                                                                                                                                               WW;
                                                                                                                                       Score 388; DB 1;
Pred. No. 7.02e-75;
37; Mismatches 96
                                                                                                                                                                                                                                                                                                                   COMPLEMENT CONTROL PROTEIN.
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 3.
                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                            E4322CC9A6EF8997 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis S.W., Winglow J.P.,
                                                                                                                                         96;
                                                                                                                                                                 Length 263;
                                                                                                                                      Indels 21;
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P04003;
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01-NOV-1997
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4B-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4BPA OR C4BP.
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"Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of the C4bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;
"Molecular cloning of the cDNA coding for proline-rich protein (PRP):
identity of PRP as C4b-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic organization protein gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Chung L.P., Bentley D.R., Reid K.B.M.;
"Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 86301119.
Lintin S.J., Reid K.B.M.;
"Studies on the structure of the human C4b-binding FEBS Lett. 204:77-81(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 203-288 FROM N.A.
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                                                                                                                                                                                                                               Chung L.P., Gagnon J., Reid K.B.M.;
"Amino acid sequence studies of human C4b-binding protein: N-terminal
sequence analysis and alignment of the fragments produced by limited
proteolysis with chymotrypsin and the peptides produced by cyanogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 80-597 FROM N.A.
"Visualization of human C4b-binding protein and vitamin K-dependent protein S and complement proproc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983)
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 49-88. MEDLINE; 85296001.
                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
                                                                              MEDLINE; 832
Dahlback B.,
                                                                                                                                                                                                               bromide treatment."
                                                                                                                                ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lett. 232:328-332(1988).
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                                                                                                                                                                                   Immuno1.
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                                                         83221615.

B., Smith C.A., Mueller-Eberhard H.J.;
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                                                                                                                                                                                   22:427-435(1985).
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27, Last sequence update)
35, Last annotation update)
IN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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on of the alpha
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        and complement protein 80:3461-3465(1983).
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165:138-144(1989).
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chain of
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                                                         its complexes with
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                                                                                                                                        BINDING
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EMBL;
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ACCENTAGE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SERIM ANTICOLD COMPLEX.

SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OF 3 POSSIBLE SORTS: A 570 KD COMPLEX OF 7 ALPHA CHAINS AND 1 BETA CHAIN, A 530 KD HOMOHEDTAMER OF ALPHA CHAINS OR A 500 KD COMPLEX OF ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE BINDING CALB AT MITT THE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M31452; AAA36507.1;
M624786, AAA36506.1;
M624776, AAA36506.1;
M624778, AAA36506.1;
M62478, AAA36506.1;
M62478, AAA36506.1;
M62479; AAA36506.1;
M62480; AAA36506.1;
M62481; AAA36506.1;
M62482; AAA36506.1;
M62482; AAA36506.1;
M62484; AAA36506.1;
M62484; AAA36506.1;
M62485; AAA36506.1;
M62484; AAA36506.1;
M62485; AAA36506.1;
M62486; AAA36506.1;
M62486; AAA36506.1;
M62486; AAA36506.1;
M62487; AAA36506.1;
M62488; AAA36506.1;
M62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A33568;
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                                                                                                                                                                                                                                                                                                   C4B-BINDING PROTEIN ALPHA CHAIN.
8 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 4.
SUSHI 6.
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Kristensen T.;
"Structure of the human beta-2-glycoprotein I gene.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                              SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=LIVER;
                                                                                  "Characterization, expression and evolution of mouse beta glycoprotein I (apolipoprotein H)."; Biochem. Biophys. Res. Commun. 200:1521-1528(1994).
                                                                                                                                          STRAIN-CBA/J; TISSUE-LIVER; MEDLINE; 94242017. Sellar G.C., Steel D.M., Za
                                                                                                                                                                                                                                                                                                                                             Q01339;
Q01339;
Q01-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-JUL-1999 (Rel. 38, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
                                                                                                                                                                                                                            Nonaka M., Matsuda Y., Shiroishi "Molecular cloning of mouse beta gene to chromosome 11.";
                                                                                                                                   Whitehead A.S.;
                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                               Genomics 13:1082-1087(1992).
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 92372000.
                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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llarity 31.5%;
Conservative
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52; 1
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Pred. No. 3.
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2-glycoprotein I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D10056; BAA00945.1; -. EMBL; S70439; AAB30789.1; -. EMBL; Y11356; CAA72190.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                   81
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                                                                                                                                                                                                                                                                                        Local
                                              NG--S-PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI
                                                                        NGYVNYPAKPVLLYKDKATFG--CHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVK 269
                                                                                                   VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI
                                                                                                                             KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFPPRPE
                                                                                                                                                        TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                   TS---FEYPKNISFACNPGF-FLNGTSSSKCTEEGKWSPDIPACARITCPPPPVPKFALL
                                                                                                                                                                                                             TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
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                                                                                                                                                                                                                                                                       18.3%;
Similarity 29.4%;
74; Conservation
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183
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                                                                                                                                                                                                                                                                                    Score 371;
Pred. No. 3.
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4 X SUSHI (SCR) REPEATS.
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3.37e-70;
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Q63514;
Q1-NOV-1997
01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural and functional relationships among human, bovine, rabbi mouse, and rat proteins.";
J. Immunol. 158:1315-1323(1997).
J. Immunol. 158:1315-1323(1997).
ACTIVATION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDBOLYZES THE COMPLEMENT FRAGMENT C4B. I ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
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SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z50051; CAA90391.1; -. P10998; 1VVC.
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35, Last sequence update)
36, Last annotation updat
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BY SIMILARITY.
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BY SIMILARITY
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8 X SUSHI (SCR) REPEATS.
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thi; Muridae;
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ae; Murinae;
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human,
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bovine, rabbit,
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         (POTENTIAL)
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADG (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                           endothelium: sequence similarity to proteins involved
adhesion and inflammation.";
cell 56:1033-1044(1989).
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Homo sapiens (Human)
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   Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
The p-selectin gene is highly polymorphic: reduced frequency of the
Pro715 allele carriers in patients with myocardial infarction.";
Hum. Mol. Genet. 7:1277-1284 (1998).
1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE
TO CARROHYDRATES ON MEDITAPELIS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
                                                                                                                                                                             Bajorath J., Stenkamp R., Aruffo A.; "Knowledge-based model building of proteins: concepts and examples."; Protein Sci. 2:1798-1810(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnston G.I., Cook R.G., McEver R.P.; "Cloning of GMP-140, a granule membrane protein of platelets and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                MEDLINE; 94093388.
                                                                                                                                                                                                                                              3D-STRUCTURE MODELING OF 42-161
                                                                                                                                                                                                                                                                              Biochemistry 35:13733-13744(1996).
                                                                                                                                                                                                                                                                                                             "Structure and function
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pred. No. 3.37e-70;
57; Mismatches 87;
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: M60234; JEMBL: M60218; JEMBL: M60219; JEMBL: M60219; JEMBL: M60223; JEMBL: M60224; JEMBL: M60224; JEMBL: M60226; JEMBL: M60227; JEMBL: M60227; JEMBL: M60227; JEMBL: M60227; JEMBL: M60229; JEMBL: M60229; JEMBL: M60229; JEMBL: M60229; JEMBL: M602231; JEMBL: M602231; JEMBL: M60223; JEMBL: M60231; JEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE CELL SURFACE.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.

DATABASE: NAME-PROW; NOTE-CD guide CD62P entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                           pF00008; EGF; 1.
; PF00059; lectin_c; 1.
pF00084; sushi; 9.
adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A30359; A30359.

1FSB; 01-APR-97.

1KJD; 03-APR-96.
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M60233; AAA35910
                       AAA35910.1; JOINED
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Q01016;
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Q1-APR-1993
15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                              61 KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                         TESG-WR-PLPSCEEKSCDNPYIPN
                                                                                                                                                                                                                                                              GHWSAPLPTCEAISCEPLESPVHGSMDCSPSLRAFQYDTNCSFRCAEGFMLRG-ADIVRC
                                                                                                                                                                                                                          GFWSKEKPKCVEISCKSPDV-INGS-PISQKI-IYKENERFQYKCNMGYEYSERGDAV-C
                                                                                                                                                                                                                                                                                                                                                                                                               QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.0%;
Similarity 26.0%;
     (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                   STANDARD;
     35,
25,
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Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 344; DB 1; Length 830;
Pred. No. 8.01e-63;
56; Mismatches 122; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                               PRT;
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/FTId=VAR_004195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_004193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_004192
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                                                                             360 AA
 update)
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**New member of the multigene family of complement control proteins herpesvirus sainti.";

**J. Virol. 66:3937-3940(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Virol. 66:3937-3940(1992).

-!- ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED FORM ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
-!- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).
-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64346; CAA45626.1; EMBL; X64346; CAA45627.1; EMBL; X60283; CAA42823.1; EMBL; X60283; CAA42822.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY TO CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaherpesvirinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpesvirus saimiri (Strain 11).
                                                                                            VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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PIR; S24567; S24567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B42534; WMBE2E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                  VARSPLIC
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Local Similarity hes 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
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83
146
209
328
84
    Conservative
                                                                                              ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sushi;
                                                                                                                         360
                          16.8%;
                                                                                                 40006 MW;

    Transmembrane; Alternative splicing;

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                             Pred.
                               Score 341; DB 1;
Pred. No. 5.23e-62;
                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
COMPLEMENT CONTROL PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUSHI
                                                                                                                    RICNGNCTTSMPTQ -> AECACPGSNYPISS
SHORT ISOFORM).
MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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Y SIMILARITY.
                                                                                                 6278A6C2ECD49669 CRC64;
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         Mismatches
                                                  Length 360;
         Indels
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            22;
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            Gaps
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01-AUG-1988 (Rel. 08, C
01-FEB-1994 (Rel. 28, I
01-NOV-1997 (Rel. 35, I
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the serum complement system.";
Biochemistry 26:4668-4674(1987).
-i- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM ANYLOID P COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cDNA structure of murine C4b-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 88024997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4BPA OR C4BP.
                                                           REPEAT
REPEAT
REPEAT
                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                     -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 DVING-SPISOKIIYKENERFOYKCNMGYE-YSERGDAVCTESGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP
                                                                                                                                                                 Complement
                                                                                                                                                                                               PFAM;
                                                                                                                                                                                                                                                       EMBL; M17122; AAA37312.1; ALT_INIT.
                                                                                                                       REPEAT
                                                                                                                                   DOMAIN
                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                         PIR; A27117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA CHAIN OF C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVFEYGVKAVYTCNEGYOLLGEINYREC--DIDG---WINDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP
                                                                                                                                                                                                             MGI:88229; C4BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                             PF00084; sushi; 6
                                                                                                                                                                                                                           P10998;
                                                                                                                                                                               pathway;
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
 SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                               Glycoprotein; Repeat; Sushi; Signal.
                                                                                                                       6 X SUSHI (SCR) REPEATS SUSHI 1.
                                                                                                                                                   C4B-BINDING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469
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Best Local
                                                                                                                                                                                                                        encoding rat P-selectin.";
Gene 145:251-255(1994).
-!- FUNCTION: CA(2+)-DEPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEM3_RAT STANDARD; PRT; 768 AA.

P98106;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                             MEDLINE; 94333817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                               Auchampach J.A., Oliver M.G., Anderson D.C., "Cloning, sequence comparison and in vivo exp
                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
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    FUNCTION: CA(2+) - DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OF PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALY:-LEWIS X.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,
LING, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.
INDUCTION: ACUTE INFLAMATION (PROBABLY).
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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llarity 28.9%;
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Pred. No. 5.23e-62;
57; Mismatches 109
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expression
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS001186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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DB 1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE HUMAN SUSHI-2 EQUIVALENT.
                                                                         POTENTIAL.
ENDOCYTOSIS SIGNAL (PROBA ENDOCYTOSIS SIGNAL (PROBA ENDOCYTOSIS SIGNAL (PROBA ENDOCYTOSIS)
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C-TYPE LECTIN (SHORT FORM).
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Length 768
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Q28065;
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metaztiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         formation with protein S.";

J. Immunol. 153:4190-4199(1994).

J. Immunol. 153:4190-4199(1994).

J. Immunol. 153:4190-4199(1994).

J. TERMINOL. 153:4190-4199(1994).

J. TERMINOL. 153:4190-4199(1994).

J. TERMINOL. 153:4190(1994).

J. TERMINOL. 153:4190(1994).

J. TOMPLEMENT OF COMPLEMENT FRACKENT COMPLEMENT FRACKENT COMPLEX (C3 ALSO ACCELERANTES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERANTES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRACKENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO MITH SERUM AMYLOID P COMPONENT.

J. SUBBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillarp A., Thern A., Dahlbaech B.;
"Bovine C4b binding protein. Molecular cloning of the alpha and
beta-chains provides structural background for lack of complex
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                        PF00084; sushi;
                                                                                                                                                                                                                                                                                                            Z31693; CAA83498.1;
P10998; 1VVC.
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65; Conse
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  C4B-BINDING PROTEIN ALPHA CHAIN.
8 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 4.
SUSHI 6.
                                                                                                                                                                                                                                                             Glycoprotein; Repeat; Sushi; Signal
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                                                                                                                                                                                                                                     SIMILARITY
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                                                                                                                                                                                                                                                                                               IT 14
LEM3_MOUSE STANDARD.

Q01102;
Q01102;
Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1999 (Rel. 38, Last annotation update)
Q1-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN MOLECULE 3) (LECAM3).

(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                                                              Weller A., Isenmann S., Vestweber D., "Cloning of the mouse endothelial selectins. Expression of both and p-selectin is inducible by tumor necrosis factor alpha."; J. Biol. Chem. 267:15176-15183(1992).
   SEQUENCE FROM N.A
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 92340571.
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Pred. No. 3.41e-61
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PRINTS; PRO0343; SELECTIN.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/pmar. usage).
                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                 REPEAT
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-!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A42755; A42755.
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PF00084; sushi; 8.
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                                                                                                                                                                                                                                                                                                                                                           Signal; Sushi; Repeat
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                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                             EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on R.W., Ballantyne C.M., Beaudet A.L.; analysis of in vivo expression of murine p-
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IN (SHORT FORM)
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Best Local
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    MEDLINE; 90226:
Li Q., Blacher
                           SEQUENCE OF 20-41. MEDLINE; 90226328.
                                                                                                                                                            Kato
                                                                                                                                                                                                                                                           "Complete primary structure of bovine localization of the disulfide bridges. Biochemistry 31:3611-3617(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
Gao B., Virmani M., Romm E.,
Appella E., Kunos G., Takacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOH_BOVIN STANDARD: PRT; 345 AA. P17690; Q28052; Q1-AUG-1990 (Rel. 15, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN
                                                                                          Biochemistry
                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                               Bendixen E., Halkier T., Magnusson
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 4-345 FROM N.A., PARTIAL SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                     fissue=plasma
                                                                                                                                                                                                                       SEQUENCE OF 20-345,
                                                                                                                                                                                                                                                                                                                                   Kristensen
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                               ., Enjyoji K.-I.; acid sequence and location of the glycoprotein I: the presence of fi mistry 30:11687-11694(1991).
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Similarity 30.0%;
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Esch F., Congote L.F.;
                                                                                                                                                                                                           CARBOHYDRATE-BINDING SITES, AND DISULFIDE BONDS
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Pred. No. 1
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                                                                                                          five
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l.83e-61;
                                                                                                                              disulfide
                                                                                                        Sushi domains.
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PIR; S09032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation from fetal bovine serum of an apolipoprotein-H-like protein which inhibits thymidine incorporation in fetal calf
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153 LSVYKPLAGNNSFYGSKAV-FKCLPHHAMFGNDTVTCTEHGNWT-QLPECREVRCPFPSR 210
                                        80 LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGK 138
                                                                                  97
                                                                                                                        22
                                                                                                                                                              39 RTYEPGEQIVFSCQPGYVSRGGIRRFTCPLTGLW-PINTL-KCMPRVCPFAGILENGTVR 96
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FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND CEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS
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                                                                                YT---TFEYPNTISFSCHTGFYLKGASSAK-CTEEGKWSPDLPVCAPITCPPPPIPKFAS 152
                                                                                                                        QTYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSUE SPECIFICITY: PLASMA
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                                                                                                                                                                                                                           Similarity
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29.1%;
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Pred. No. 4.13e-60;
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15-FEB-2000 (Rel. 39, Last annotation update)
MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P15529;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cervoni F., Fenichel P., Akhoundi C., Hs:
"Characterization of a cDNA clone coding
cofactor protein (MCP, CD46).";
cofactor protein (MCP, CD46).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 82286080.

Lublin D.M., Liszewski M.K., Post T.W., Arce M.A., le Beau M.M., Lublin D.M., Lemons R.S., Seya T., Atkinson J.P.; Rebentisch M.B., Lemons R.S., Seya T., Atkinson of human membrane "Molecular cloning and chromosomal localization of human membrane "Molecular cloning and chromosomal localization in the multigene
          Purcell D.F., Russell S.M.,
McKenzie I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cofactor protein (MCP). Evidence for inclusion in the multigene family of complement-regulatory proteins ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 I-VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK--S- 194
                                                                                                                                                                                                                                                                              "Characterization of the promoter region of the membrane cofactor protein (CD46) gene of the human complement system and comparison to a membrane cofactor protein-like genetic element.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                           Russell S.M., Sparrow R.L., McKenzie I.F.C., Purcell D.F.J.; "Tissue-specific and allelic expression of the complement regulator
                                                                                                                                                                                                                                                                                                                                                                                             regulator of complement activation. Immunogenetics 33:335-344(1991).
                                                                                                                                                                                                                                                                                                                                                                                                          "Alternatively spliced RNAs encode several isoforms of CD46 (MCP), regulator of complement activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 PDNGFVNHPANPVLYYKDTATFG--CHETYSLDGPEEVECSKFGNWSAQPSCKA-SC
                                                                                                                                                                                  CD46
                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                      ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                          mmunogenetics
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                                                                                                                                                                                                                                                                 Immunol. 151:4137-4146(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDV-INGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reprod. Dev. 34:107-113(1993).
                                                                                                                                                                                                                                                                                                                                     Hourcade
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 ISOFORM (TRANSCRIPTS A AND B) IS PREFERENTIALLY EXPRESSED IN
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                                                                                                                                                                                                                                                                                                                                    D., Post T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 35-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deacon N.J., Brown M.A.,
                                                                                                                                                                                                                                                                                                                                       Greenlund A.C., Atkinson J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377
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                              Matches
                                        Query Match
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MTM; 120920;
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                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y00651; CAA68675.1; --
EMBL; S51940; AAB24802.1; --
EMBL; M58050; AAA62833.1; --
EMBL; A18585; CAA01400.1; --
EMBL; S65879; AAD13968.1; --
                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S01896; S01896.
33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
                          Local Similarity nes 81; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EBV-B CELLS AND LEUKEMIC CELLS. THE 66 KD ALPHA ISOFORM AND THE 56 KD BETA ISOFORM FOUND IN ALL TISSUES EXCEPT SPERM CORRESPOND TO THE TRANSCRIPTS C AND D, AND THE TRANSCRIPTS E AND F RESPECTIVELY. THE EXON 9 IS SPECIFICALLY DELETED IN SOME PLACEMYAE. THE EBSILON ISOFORM CORRESPONDS TO THE TRANSCRIPTS I AND J. SPERMATOZOA DELTA ISOFORM (TRANSCRIPT N) DELETE BOTH EXONS 12 AND 13. ALL TISSUES DIFFERENTIALLY SPLICE EXON 13.

TISSUE SPECIFICITY: EXPRESSED BY ALMOST ALL CELLS EXCEPT ERYTHROCYTES AND SOME BONE MARROW CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: EXTENSIVELY O-GLYCOSYLATED IN THE SER/THR-RICH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE: NAME-PROW; NOTE-CD guide CD46 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd46.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATABASE: NAME-PROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Alternative
                                                                         377 AA;
                                                                                                                                                                    Conservative
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31.0%;
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                                                                         MW;
                          Score 335; DB 1;
Pred. No. 2.22e-60;
54; Mismatches 99
                                                                                                  TYLIDETHREVEFISL -> KADGGAEYATYQIKSTI
RG (IN ISOFORM B/D/F/H/J/L).
MISSING (IN ISOFORM MAND ISOFORM N).
MISSING (IN ISOFORM N).
I -> IGKOMUFILMMOITED MODIFORMS.
                                                                                                                                                   MISSING (IN A SECOND FORM).
MISSING (IN ISOFORM M).
YLORRKKKG -> DIFKGGRRKGKOMVELNMPLTRLNOPLQ
OSREAE (IN ISOFORM M).
                                                                                                                                                                                                                                                                                                                                                                 4 X SUSHI (SCR) REPEATS SUSHI 1.
SUSHI 2.
                                                                                    ISOFORM
                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                       SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                            SUSHI
                                                                                                                                                                                                                                                                                                                                                        SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE COFACTOR PROTEIN
                                                                       2CA6F61752570B57 CRC64;
                                                                                                                                                                                                                                      SIMILARITY.
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                          99;
                                               Length 377;
                                                                                                                                        KADGGAEYATYQTKSTTPAEQ
                        Indels 27;
                       Gaps
                        22;
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RESULT

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MEDLINE; 92135065.
Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K., Yasuda T., Koike T.:
"Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) cDNA cloning and inter-species differences of beta 2-GPI in
                                                                                                                                                                                                                   Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N., Werner P., Arnaud P.; "Molecular cloning and sequence analysis of the cDNA encoding huapolipoprotein H (beta 2-glycoprotein I).";
                                                                                                                                                                                                  apolipoprotein H
Int. J. Clin. Lak
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21-JUL-1986 (Rel. 01, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 92273779.
                                                                                                                                                                                                                                                                                                                                                                                                                                              apolipoprotein
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and expression of the human apolipoprotein H (beta 2-glycoprotein I).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LIVER;
MEDLINE; 92084151.
Mehddi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,
Peeples M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen Moller K.B., Hundahl Moller N.P., Sottrup-Jensen L.; "Molecular cloning and mammalian expression of human beta 2-glycoprotein I CDNA,"; FEBS Lett. 289:183-186(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steinkasserer A., Estalle "Complete nucleotide and glycoprotein I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                108:293-298(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E=LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277:387-391(1991).
                                                                                                                                                                                                        Lab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                     Res.
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"Complete amino acid sequence of human plasma beta 2-glycoprotein I.";
Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
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Hum. Genet. 100:57-62(1997).
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Hum. Genet. 91:401-402(1993).
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MEDLINE; 93050249.
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Identification of structural mutations in the fifth domain of
apolipoprotein H (beta-2-glycoprotein I) which affect phospholipid
binding.";
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-!- FUNCTION: BIN
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 or send an email to license@isb-sib.ch).
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FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN. PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.

TISSUE SPECIFICITY: PLASMA.

SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
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Search completed: Thu Jun 8 21:42:12 2000 Job time: 13 secs.

Description: Perfect Score: Run on: MPsrch_pp Sequence: Tabular output not generated. Database: Post-processing: Minimum Match 0% Listing first 45 summaries Scoring table: Statistics: Searched: Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm PAM 150 Gap 11 >US-09-316-163-10 (1-265) from US09316163.pep 2029 Thu Jun 8 21:42:31 2000; MasPar time 26.07 Seconds 704.848 Million cell updates/sec 1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK, 265 225878 segs, 69334122 residues Nean-43.031; Variance 62.408; scale 0.690 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_fivertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

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SUMMARIES

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            Q91275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOAMES C.J., DAY A.J., SIM R.B.;
"Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
Biochem. J. 315:523-51(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q28085;
Q28085;
                                                                                                                           260
                                                                                                                                                                               187 RP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X98697; CAA67257.1; -. HSSP; P10998; IVVC.
                                                                                                                                                                                                                       200 GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDY 259
                                                                                                                                                                                                                                                                        127 GOAVLPKATYKONERVOYRCAAGFEYGORGDTVCTKSGWTPAPTCIEITCDPPRIPNGVY 186
                                                                                                                                                                                                                                                                                                                                      140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                          67 FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LAEGNOFEYGAKVVYTCDEGYOMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPENGKI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 46.98;
Local Similarity 64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNYIMVCRKGEWVALNPLR 78
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                                                                                                                        SP 261:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKEKPKCYEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPSCEEKSCDNPYIPNGDYSPLRIK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00084; sushi; 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117;
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669 AA;
      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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; 75683 MW; FAF0D174 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 952; DB 6; Length 669; Pred. No. 4.00e-230; 29; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.00e+00;
0; Mismatches 0;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
1053 AA.
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                                                Query Match
Best Local
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                                                                                                                      herpesvirus 8.";

herpesvirus 8.";

J. Virol. 73:3040-3053(1999).

EMBL; AF083501; AAD21332.1; -.

SEQUENCE 645 AA; 71526 MW;
                                                                                                                                                                                                                   MEDIJINE: 99174001.

MEDIJINE: 99174001.

SEARLES R.P., BERGQUAM E.P., AXTHELM M.K., WONG S.W.;

"Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPTENS:
neblifer).";
neblifer).";
Biochem. J. 301:391-397(1994).
EMBL; L21703; AAA92556.1;
EMBL; L21703; AAA92556.1;
HSSP; P08603; 1HFH.
PFAM; PF00084; Sushi; 16.
PFAM; PF00084; Sushi; 16.
1053 AA; 117597 MW; ODF68EDB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta rhadinovirus 17577.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9WRU2;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
21.5%;
Local Similarity 30.9%;
es 72; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 GDYSP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 SSAMEPDREYHFGOAVREVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement_regulatory plasma protein from barred sand bass (Parablax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paralabrax nebulifer (barred sand bass).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Reposterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Serranidae; Paralabrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 TRYEP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 GSPISQKIIYKENERFQYKCNMGYEYSERGDA-V--CTESGWRPLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQV 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAHMEN A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94318039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
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      Score 436; DB 14; Length 645; Pred. No. 2.63e-85; 50; Mismatches 94; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Mismatches 101; Indels 12;
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                                                                                                                                60FB82D6 CRC32;
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Indels 17;
Gaps
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040912;
01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999
ORF 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U93872; AAB62602.1; -. HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIPEL F., ALBRECHT J.C., FLECKENSTEIN B.;
"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
J. VICOL. 71:4187-4192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 97296220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                           Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                        P88903;
                                                                                                                                                                         P88903
                                                                                                                                                                                                                                                                                                                                                                                          110 ANISYVCNEGYFLVGREYVRYCMIGASGOMAWSSSPPFCEKEKC-H-R-P---KIENGDF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
   SEQUENCE FROM N.A. MEDLINE; 97121480.
                                            Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                                                                                             \mathfrak{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 RCRSGYTTYARNITATCLQGGTW-S-EPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 20.8%;
Local Similarity 31.9%;
es 75; Conservative
                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITNGKY--HPVK-DF-YQYLDTVTFSCNRDFSLVGDEMTTCISNT-WNKPFPRCEQITCS 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTGG-NVFEYGVKAVYTCNEGYQLLGE-IN-Y--REC-DTDGWINDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTSGEDAFKYGTNITYKCNEGYQLLGSMVRICMLKDDLKTVDWEPKAPICDIEKCKPPPQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKYSVGASVELICRPGFTKMOSTVSVECLSNGTWTAPNA--KCHRKKCPTPQELLNGEYI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APNIAHGKLLTGSSSVYKYGQSVTIGCETGFTLIGSEISTCKDSSWDPPLPTC 562
                                                                                                                                                                                                                                                                                                  EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
                                                                                                                                                                                                                                                                                                                                KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI 223
                                                                                                                                                                                                                                                                                                                                                               VKAVYTCNEGYQLLG-E-INYRECDTDG---WINDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                   SQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                  QGFSLTYKHKQSVTFACNDGFVLRGSPTITCNVTEWDPPLPKCVLEDIDDPNNSN 278
                                                                                                                                                                                                                                                                                                                                                                                                                             KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBLrel. 05, Created)
(TremBLrel. 05, Last seq
(TremBLrel. 12, Last ann
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 422; DB 14;
Pred. No. 1.61e-81;
46; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                              550 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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EMBL; U75698; AAC57082.1; -.
HSSP; P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOORE P.S., BASHOFF C., WEISS R.A., CHANG Y.;
"Molecular mimicry of human cytokine and cytokine response pathway genes by KSHV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA D., PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00084; sushi; 4
SEQUENCE 550 AA; 6068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY 1997 (TrEMBLrel. 03, Created)
01-MAY 1997 (TrEMBLrel. 03, Last sequence update)
01-MOV-1999 (TrEMBLrel. 12, Last annotation update)
41KBP FRAGMENT FROM LEFT END OF GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D17L OR C17L.
Cowpox virus (CPV).
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                                                                                                                                                                                                         SHCHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A., RYAZARKINA O.I., GUTOROV V.V., KOTWAL G.J.; The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 97068532.
SAFRONOV P.F., PETROV N.A., RIAZANKINA O.I., TOTMENIN A.V., SHCHELKUNOV S.N., SANDAKHCHIEV L.S.; "Genes of a circle of hosts for the cowpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-GRI-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-GRI-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI 223
                                                         EMBL; X94355; CAA64102.1; -. EMBL; Y11842; CAA72567.1; -. HSSP; P10998; IVVC.
                                                                                                                                                   proteins.";
Virology 243:432-460(1998).
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98229462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 SQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSCEEKSCDNPYIPN 256
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%;
Local Similarity 31.9%;
es 75; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 RCRSGYTTYARNITATCLQGGTW-S-EPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKAVYTCNEGYQLLG-E-INYRECDTDG---WINDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-H-R-P---KIKNGDF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
PF00084; sushi; 4.
NCF 259 AA; 28193 MW;
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Pred. No. 3.00e-81;
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            76531F63 CRC32;
                                                                                                                                                                                                                                                                                                                                          TOTMENIN A.V., PETROV N.A.,
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      DAY A.J., RIPOCHE J., LYONS A., MCINT "Sequence analysis of a cDNA clone en human complement factor H.", Biosci. Rep. 7:201-207(1987).
EMBL; M17517; AAA52016.1; -.
HSSP; P08603; 1HFH.
PFAM; PF00084; sushi; 11.
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Best Local
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Q14006;
239 RPLPSCEEKS--CDNPY-IPNGDYSPLRI 264
                             523 TEPPQCKDSTGKCGPPPPIDNGDITSFPL 551
                                                                    182
                                                                                                 465
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                                                                                                                                                            409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENT H FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 1), Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                          352
                                                                                                                                                                                                                                                           296 CSQ-PPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKW-S-SP-PQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 NPEAPICESVKCQSPPSISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGYLCSG 188
                                                                                                                                                                                                                                                                                                          I9.5%;
Local Similarity 27.5%;
es 74; Conservation
                                                                                                                                                                                                                                           3 CNELPPRRNTEILTGSWSDQ-TYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 QCIKRRCPSPRDIDNGQLDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                       KEKPKCVEISC-KSPDVINGSPIS-QKIIYKENERFQYKCNMGYE-YSERGDAVCTESGW
                                                                                   -GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGERVRYQCRSPYEMFGD-EEVMCLNGNW 522
                                                                                                                  ICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWS 181
                                                                                                                                              SCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQVTYTCATYYKMDGASNVTCINSR-WT 464
                                                                                                                                                                              CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIP 121
                                                                                                                                                                                                CEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKCFEGFGIDGPAIAK-CLGEKWSHP-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGFWSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GE-WS-DPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG-WRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNTWQPELPKC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCPIPSRPITMKFKGT-VDSHYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                          657 AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.6%;
ilarity 34.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYONS A., MCINTOSH B.,
                                                                                                                                                                                                                                                                                                     Score 396; DB 4; Length 657;
Pred. No. 1.60e-74;
64; Mismatches 111; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 398; DB 14; Length 259;
Pred. No. 4.65e-75;
39; Mismatches 104; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                          F4AB5238 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding the C-terminal end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 22;
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q89859; PRELIMIN...
Q89859; Q8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
              MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.; Submitted (JUL-1995) to the EMBL; L22579; AAA60760.1; - EMBL; U18340; AAA69423.1; - EMBL; D1938; 1VVC.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BANGLADESH-1975;
MEDILINE; 94088747.
MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
MASSUNG R.F., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREY V.N.;
"Potential virulence determinants in terminal regions of variola
                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SOMALIA-1977;
                                                                                                                                                                                                                                                                 smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orthopoxvirus
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Q9YTQ8;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1998) to the EMBL/GenBank/DDBJ EMBL; AF083424; AAC95530.1; -HSSP; P10998; TVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 CKSPDVINGSPISQKIIYKENERF-QYKCNMGYEYSERGDAVCTESGWRP-LPSCE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 CKIPOVANGHVEVRKTSNNVQYQYVNIKCDKGFRLQGETPNMCKNGVWFPALPTCE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Primary Structure of the Herpesvirus Ateles Genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 ANGT--HTNIK-E-YYTYLDAVTYSCNDETKLTLTGPSSKQCSETGRWVPDEETKCEFKV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 SDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 SSGSYPNGTTLQVTCRKGYIGRQIQTVTCVNGNW-TV-P-NECQKRRCSTPADLLNGWYT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTGGNVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WTNDIPICEVVKCLPVTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTG-NLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRVNWTPRPPICEITKCKPPPTI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o
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82; Conser
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sushi; 4.
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39; ]
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Pred. No. 8.91e-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poxviridae; Chordopoxvirinae;
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                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q07033 PRELIMINARY; PRT; 263 AA. G07033; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                SHCHELKUNOV S.N., BLINOV V.M., RESENCHUK S.M., TOTMENIN A.V., OLENINA L.V., CHIRIKOVA G.B., SANDAKHCHIEV L.S.;
"Analysis of the nucleottde sequence of 53 kbp from the right of the genome of variola major virus strain India-1967.";
"Yrus Res. 34:207-236(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SHCHELKUNOV S.N., BLINOV V.M., "Genes of variola and vaccinia protective mechanisms."; FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=INDIA-1967, SSP. MAJOR;
MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variola virus.
Viruses; dsDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D12L PROTEIN D12L.
                                                                                                                                                                       SHCHELKUNOV S.N., TOTMENIN A.V.;
"Two types of deletions in orthopoxvirus Virus Genes 9:231-245(1995).
EMBL; X69198; CAA48953.1; -.
PIR; C36838; C36838.
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-INDIA-1967, SSP. MAJOR;
MEDLINE; 95320969.
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=INDIA-1967, SSP. MAJOR;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193
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 97
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                                                        40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGH 96
                                                                                      Local Similarity
nes 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT
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 LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                            SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                              PF00084; sushi; 4.
NCE 263 AA; 28789 MW;
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                                                                                     17.6%;
larity 33.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 357; DB 14; Length 263; Pred. No. 3.96e-64; 38; Mismatches 95; Indels 23;
                                                                                                 Score 357; DB 14;
pred. No. 3.96e-64;
                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C9DFBA61 CRC32;
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                                                                                                                                                6436C44C CRC32;
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                    genomes.";
                                                                                                                   Length 263;
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                                                                                         Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overcome the host
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                                                                                           Gaps
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Q89076;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Q22328
Q22328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variola virus
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOH
                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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                                                                                                          STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                      T07H6.5
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                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS-NGR--HNGYN-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IS-NGR--HNGYN-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC
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Similarity 33.6%;
79; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA;
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. 01, Last sequence. 12, Last annotation.
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Last annotation update)
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---- No. 1.34e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                              Secernentea; Rhabditia; Rhabditida;
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                                                                                                                                                                                                                             Caenorhabditis
                JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                   COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
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Best Local
                                                                                                                                                                                  EMBL; U75654; AAC13888.1;
HSSP; P10998; 1VVC.
PFAM; PF00084; Sushi: 7
         SEQUENCE
                                                                                                                                                                                                                                                                                                                    binding proteins.";
J. Biol. Chem. 272:12714-12722(1997)
                                                                                                                                                                                                                                                                                                                                                                                       "AM67, a secretory component of the guinea pig sperm acrosomal matrix, is related to mouse sperm protein sp56 and the complement component 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrembLrel. 04, Created)
01-JUL-1997 (TrembLrel. 04, Last sequence update)
01-NOV-1999 (TrembLrel. 12, Last annotation update)
ACROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOSTER J.A., FRIDAY B.B., MAULIT M.T., BLOBEL C., WINFREY V.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97284752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-HARTLEY; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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STRAIN-BRISTOL N2;
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LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMERS D., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Local Similarity 32.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDAVCTESG-WR-PLPSCEEKSCDNPYIPNG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEMHCSDDGFWSKEKPKCVEISCKS-PDVINGSPISQKIIYKENERFQYKCNMGYEYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE 110
533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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59772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches 82; Indels 19;
                            POTENTIAL.

ACROSOMAL MATRIX COMPONENT AM67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 353; DB 5;
Pred. No. 4.52e-63;
60EEA526 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 AA
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Best Local Similarity 27.0%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-CONGO-1965;

MASSUNG R.F., LOBAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,

TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

EMBL; U18337; AAA69317.1; -.

HSSP; P10998; IVVC.

PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q89061;
Q89061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variola virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                   133 APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
193 KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                     207 PHPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSLSSTCSPGNTWQPELPKC 261
                                                                                                                                                                                                                                                                                                          78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-Y-RECDTDG--WINDIPICEVVKC-LPVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEKS 248
                                                                                                                                                                                                                                                                                                                                                                                   97 LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 C-DNPYIP 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                        IS-NGR--HNGYN-DF-YTDGSVYTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGK-HSGT-DEDL-YTYGSLVTYVCDPNYSLLGNASISCLVANKTVGVWSSNPPTCEKVI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIT-DLL-FGSTIEFSCSKGYSLIGSTT-SQCESQGKTVDWSDPLPECVIVKCDSPPDIS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETNFRTGTALKYNCHRGYWRVNSSHVICDINGSWI-YNVF--CAKKRCRNPGELANGKVE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRQPHIPKGIFLSGFGFYYTYKDTLVISCKKGYILRGSSIIHCEANSKWYPSIPTCEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHC--SDD--GFWSKEKPKCVEIS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTAPE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.28;
33.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 350; DB 14; Length 263; Pred. No. 2.81e-62; 37; Mismatches 96; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 351; DB 11;
Pred. No. 1.53e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Mismatches 93; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55866165 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps 16;
```

Search completed: Thu Jun Job time: 30 secs.

8 21:43:01 2000

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Jun 8 21:44:51 2000; MasPar time 11.39 Seconds 684.453 Million cell updates/sec

>US-09-316-163-11 (1-329) from US09316163.pep 2539

Description: Perfect Score:

Sequence: 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 329

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Watch 0% Lighting first 45 summaries

i-geneseq36 . 1::geneseqp

Database:

Mean 33.142; Variance 124.795; scale 0.266

Statistics:

pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 5 5 5 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
1183 14520 14520 1409 1409 1400 1400 1400 1400 1400 140	Score
72. 2 17. 8 17. 8 17. 8 17. 1 16. 1 16. 1 16. 1 16. 0 16. 0 16. 0 15. 9 15. 9 15. 7 15. 7 15. 7 15. 7 15. 7	Query Match
240 578 578 290 290 290 290 200 200 200 200 200 200	Length
	DB
W39154 Y09065 Y09065 Y09065 Y09065 W39156 W39156 W39157 W45899 P945899 R11810 R28557 R285557 R285557 R285557 R285557 R285557 R285557 R285556 R285556	ID
Human partial Compleme Clone pRRB9FH410 CFH r Human C4 binding prote Human C4 binding prote Human C4 binding prote Human c4 binding prote Human caid sequence of Human compleme Amino acid sequence of Human complement recep CRI-4 (85%, 87%) analogue. CRI-4 (1145) analogue. CRI-4 (1991, 1035) analogue. CRI-4 (369-376 STKPPIC CRI-4 (52%, 53%, 54P) CRI-4 (364-367 NAAH) a CRI-4 (197) analogue.	Description
13.40e-190 9.41e-169 9.41e-169 9.41e-36 3.96e-31 3.96e-31 1.369e-31 1.369e-33	Pred. No.

Query Match 72.2%; Score 1832; DB 1; Length 240; Best Local Similarity 100.0%; Pred. No. 3.40e-190; Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

Ş В Qy B

121 INGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNG 180

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45	44	43	42	41	40	39	38	37	36 6	35 51	34	33	32	31	30	29	28	27	26	25	24	1
341	362	371	376	382	382	385	385	386	387	389	391	390	391	393	393	393	393	394	394	395	395	
13.4	14.3	14.6	14.8	15.0	15.0	15.2	15.2	15.2	15.2	15.3	15.4	15.4	15.4	15.5	15.5	15.5	15.5	15.5	15.5.	15.6	15.6	
302	579	263	830	577	543	543	543	543	543	543	2039	543	543	543	543	543	543	543	543	543	543	
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R55793	W39924	P92003	R65216	W06882	R28546	R28559	R28543	R28554	R28556	R28564	R36743	R28548	R28544	R28562	R28570	R28566	R28545	R28551	R28561	R28563	R28549	
Herpesvirus saimiri sc	sequence of	8		Membrane co-factor pro	CR1-4 (44T, 47D, 49L)	-4 (114-1	37Y) analo	-4 (92T, 94H) analo) analogue.	-4 (116K, 117P) ana		-4 (57V, 59K) analo	-4 (35E) analogue.) analogue.	-4 (266-274 KLKTQTN	-4 (318R, 319N) ana	-4 (37Y) analogue.	-4 (65T) analogue.	4	-4 (117P) analogue.	-4 (64K, 65T) analo	
b.//e-24	4.056-25	4.50e-2/	1.32e-2/	3.04e-28	3.04e-28	1.45e-28	1.45e-28		8.90e-29	5.446-29	3.336-29	4.266-29			2.046-29				1.598-29	1.25e-29	1.25e-29	

388888 8	88	86	38	Sq	ΡT	ΡŢ	DR !	DR	ΡI	PA	PR	PR	PR	PR	ΡF	PD	PN	SO	×Σ	ΚW	DE	ğ	AC	RESULT
treatment of renal or unogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell. Sequence 240 AA;	antigens isolated from clone pRBB9FH410 (see W39155). The detection or	in the identification of complement factor H related proteins and	This partial protein sequence represents a region of the human	H related antigen, or nucleic acid encoding it	by modulating or detecting tumour associated human comprement factor	Treating or screening for cancer, e.g. renal or urogenital cancer	N-PSDB; V02790.	512742/47.	Enfield DL, Hass GM, Kinders RJ;	(BARD-) BARD DIAGNOSTIC SCI INC.	06-MAR-1997; US-038614.		09-APR-1996; US-015083.	06-MAR-1997; US-812481.	09-APR-1997; U05710.	16-OCT-1997.	WO9738136-A1.	Homo sapiens.	urogenital cancer; medicament; modulator.	Complement factor H; tumour associated antigen; renal cancer;	a 1	27-APR-1998 (first entry)	W39154;	LT 1 W39154 standard: Protein: 240 AA.

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RESULT YOU AC YO
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IN THE SULT
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09-APR-1997: U5-812481.
09-APR-1996: US-015083.
09-APR-1996: US-030048.
06-MAR-1997: US-038014.
(BARD-) BARD DIAGNOSTIC SCI INC.
Enfield DL, Hass GM, Kinders RJ;
WPI: 97-512742/47.
N-PSDB; V02791.
                                                                                                                                                                                                      06-JUL-1999 (first entry)
Human complement factor H homolog protein.
Human complement factor H; immunological mechanism; complement reaction;
gene therapy; immune stimulation; haematopoissis regulation; chemotactic;
tissue growth activity; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H related antigen, or nucleic acid encoding it
Example 6B; Fig 6B; 104pp; English.
This partial protein is found in clone prabbr#410 and represents a complement factor H related protein with homology to a region of the human tumour associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                         15-APR-1999.
02-OCT-1998;
                                                                                                                                                                                 secretory signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Y09065 standard; Protein; 578 AA. Y09065;
                                                                                                         WO9918200-A1.
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1998 (first entry)
Clone pRRB9FH410 CFH related protein fragment.
Complement factor H; tumour associated antigen; renal cancer; urogenital cancer; medicament; modulator.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a medicament for t
Sequence 216 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 QCRNGFYPATRGNTAKCTSTGWIDADRCTLKPCDYP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9738136-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCNEGYQLLGEINYRECDTDGWTNDIPICEYVKCLPYTAPENGKIVSSAMEPDREYHFGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDBITY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVRFYCNSGYKIEGDEEMHCSDDGFWGKEKPKCVEISCKSPDVINGSPISQKIIYKENER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 65.0%;
Similarity 99.5%;
                             J04448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1650; DB 1;
Pred. No. 1.47e-169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                      region
                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            short consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This DNA encodes a protein having homology to human complement factor H, which plays a role in the immunological mechanism involving the complement reaction. The protein can also be used as an antigen for preparing antibodies against the protein. The cDNA can be used as a probe for gene diagnosis and the gene for gene therapy, as well as for large-scale expression of the protein. The protein may also have immune stimulating or suppressing activity, haematopoiesis regulating activity, tassue growth activity, activin/inhibin activity, anti-inflammatory activity, tumour inhibition activity, chemotactic/chemokinetic activity, receptor/ligand activity, etc. The protein is identified by the presence of a hydrophobic N-terminal secretory signal region, knowledge of the protein function is not required, as in e.g. methods of expression
                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human C4 binding protein.
C4bp; monomer; complement protein; pJOD.C4bp.3; SCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R13490 standard; Protein; 581 AA. R13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1991
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Human proteins with secretory signal sequences and nucleotide sequences, useful in control of proliferation and differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-1997; JP-272837.

(PROT-) PROTEGENE INC.

(SAGA) SAGAMI CHEM RES CENT.

Kato S, Sekine S;

WPI; 99-264019/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 ENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claims 1; Page 55-58; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 ENTRRPYFPV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 LRIK-HRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRC-TLKPCDYPDIKHGGLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 HFGQAVRFYCNSGY-KIEGDEE--MHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 ILNEETQYNCKPGYATADGNSSGSITCLQNG-WSTQ-PICIKF-CDMPVFENSRAKSNGM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 YTCNEGYQLL-GEI-NYRECDTDGWTNDIPICEVVKCL-PVTAPENGKIVSSAMEPDREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 YYCDQNFVTPSGSYWDYIHCTQDGWSPTVP-C-LRTCSKSDVEIENG-FIS---ESSSIY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 32.8%; es 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPOKVYLPWSRVEYOCOS-YYELOGSKYVTCSNGDWSEPPRCISMKPCEFPEIOHGHLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFKLHDTLDYECYDGYESSYGNTTDSIYCGEDGWSHLPTCYNSSESCGPPPPISNGDTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat.
                                 /label= SCR5
280. .345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                        /label= SCR6
                                                                                                                                                                                                                                                                                                                    'label= SCR8
                                                                                                                                                                                                                                                                                                                                                                                                    'label= C4bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= signal_peptide
                                                                                                                                                                                                                                        label= SCR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8%;
                                                                                                                                                                                                                                                                              .155
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Pred. No. 9.41e-36;
56; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 578;
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Gaps 20;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT New C4 binding protein fusion proteins and DNA encoding them PT New C4 binding protein fusion proteins and DNA encoding them PT comprise assemblies of C4bp monomers linked to functional moiety, protein is a delivery vehicles in diagnosis and therapy PS Example 1; Fig 1; 105pp; English.

CC Distance of Fig 1; 105pp; English.

CC obtained following PCR amplification. The protein is a monomer CC containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCR, CC the first cysteine residue bonds with the third and the second CC systeine residue bonds with the fourth. This secondary structure is CC responsible for the conformational flexibility of the C4bp monomer. CC or a specified subfragment of it, e.g. having 5, 4, 3 or 1 SCR(s) CC is fused to the C-terminal of a protein such as a viral receptor, CC cell ligand, a bacterial, viral or parasitic immunogen, enzyme, CC cytokine, toxin, etc. See also Q13243-51.
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(BIOG-) BIOGEN INC.
W39156 standard; Protein; 290 AA W39156; 27-APR-1998 (first entry)
                                                                                                                                                                                                                                      191
                                                                                                                                                                                                                                                                                                                                                                                                       108 VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%;
Local Similarity 29.8%;
nes 97; Conservation
                                                                                                                                    342
                                                                                                                                                                                                                                                                                                                                                                         78 FILIGGNVFEYGVKAVYTCNEGYQLLGEINYR-EC-DID-GWINDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 107
                                                                                                                                  OGCEALCOPEPKLNNGEITQHRKSRP 367
                                                                                                                                                                                                                               SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                           SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                    TCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEPN 281
                                                                                                                                                                                                                                                                                                        ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-D-D--GFWSKEKPKCVEI 190
                                                                                                                                                                                                                                                                                                                                       RNGR--HSG-E-ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI 221
                                                                                                                                                                                                  SCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGYKPTTDEPTTVICQKNLRWTPY 341
                                                                                                    PRCTLKPCDYPDIKHGGLYHENMRRP 325
                                                                                                                                                                  SCDN-PYIPNG--D-YS-PLRIK-HRTGDEITYQCRNGFYPATRGNTA-KC-TSTGWIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winkler G, Liu TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ00567
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/label= sc
107
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724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= C4bp_core
/note= "responsible for multimer assembly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1abel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "intradomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 433; DB 1; Le Pred. No. 1.05e-33; 68; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This partial protein sequence represents a region of the human the tumour-associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens from clone prassprey210 (see w3915.7-w39159). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.

Sequence 290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BARD-) BARD DIAGNOSTIC SCI INC.
Enfield DL, Hass GM, Kinders RJ;
WPI; 97-5112742/47.
N-PSDB; V02792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1996; US-630048
06-MAR-1997; US-038614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1997; U05710.
06-MAR-1997; US-812481.
09-APR-1996; US-015083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human partial complement factor H protein fragment 2. Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H related antigen, or nucleic acid encoding it Example 6B; Fig 7B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               urogenital cancer; medicament; modulator.
                                                                                                                                                29-JAN-1999 (first entry)
Amino acid sequence of the soluble complement receptor 1 (sCR1).
Human; soluble complement receptor 1; sCR1; T-cell; B-cell;
mediated immune response; inhibition; tissue rejection; gene therapy;
dystrophin; inflammatory response; interferror-gamma secretory response;
autoimmune response; neurological response; Alzheimer's disease;
parkinson's disease; multiple sclerosis; systemic lupus erythematosus;
rheumatoid arthritis; myasthenia gravis; epidermis bullosa;
                                                                                                                                                                                                                                                                                                    W73147 standard; protein; 778 W73147;
                                                                                            Homo sapiens.
W09845430-A1.
                                      06-APR-1998; G01012.
05-APR-1997; GB-006950.
                                                                                                                              Hashimoto's disease.
  (CHER/)
                    (ANNE/) ANNENKOV A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEGFGIDGPAIAK-CLGEKWSHP-PSCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFRISEENETTCYMGKW-S-SP-PQCEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYTCATYYKMDGASNVTCINSR-WT-GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGER 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTC 96
                                                                                                                                                                                                                                                                                                                                                                                                      DEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                      SSVEYQCQN-LYQLEGNKRITCRNGQWSEPPKC-LHPC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRYQCRSPYEMFGD-EEVMCLNGNWTEPPQCKDSTGKCGPPPPIDNGDITSFPLSVYAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQYKCNMGYE-YSERGDAVCTESGWRPLPSCEEKS--CDNPY-IPNGDYSPLRIK-HRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC-KSPDVINGSPIS-QKIIYKENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.1%;
Similarity 27.0%;
    CHERNAJOVSKY Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 409; DB 1;
Pred. No. 3.96e-31;
63; Mismatches 119
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                                                                                                                                                               22-JAN-1998.
08-JUL-1997; E03715.
15-JUL-1996; GB-014871.
(ADPR-) ADPROTECH PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human complement receptor 1 (residues 1-1929).

Membrane binding element; thrombotic disease; soluble protein;
complement-related disease; integral membrane protein; inflammation;
short consensus repeat; SCR 1-3; CR1; complement receptor type 1.
                               Derivatives of soluble poly:peptide(s) bonded to low affinity membrane binding groups - useful for treating complement-rela
          thrombotic
                                                                                                                                             Dodd I
                                                                                                                                                                                                                                                                                                            WO9802454-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            Cross_links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W45899 standard; peptide; 1930 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory responses such as rheumatoid arthritis
Disclosure; Fig 1, 54pp; English.
This is an amino acid sequence of the human soluble complement receptor 1 (SCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or B-cell-mediated immune response to prevent immune response-mediated tissue rejection and destruction or clearance or inactivation of an expressed protein especially from cells that have been treated by gene therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W45899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an interferon-gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, epidermis bullosa or Hashimoto's disease.

Sequence 778 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Annenkov A, Chernajovsky Y; WPI; 98-568350/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
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                                                                                                      I, Mossakowska DEI, Smith RAG; 98-110524/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 355
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97; Conservation
          diseases,
                                                                                                                                                                                                                                                                                                 /note= "Disulphide linked to Cys in peptide given in W45889"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
   providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Mismatches 110; Indels 36;
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Pred. No. 3.96e-31;
improved
treating complex red localisation
                        complement-related
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PS Claim 22; Pages 60-61; 75pp; English.
CC This sequence represents human complement receptor 1 (CR1, CD 35)
CC This sequence represents human complement receptor 1 (CR1, CD 35)
CC N-terminal fragment. The invention relates to a soluble derivative (A)
CC of a soluble polypeptide (I), which comprises at least 2 heterologous
CC membrane-binding elements (MBE) of low membrane affinity covalently
CC associated with (I). MBE interact, independently and with thermodynamic
CC additivity, with components of cellular or artificial membranes exposed
CC to extracellular fluids. (A) are used to treat disorders treatable with
CC (I) itself, specifically inflammation or any other complement-related
CC disorder (e.g. neurological disease, graft rejection, myocardial
CC inflarction, sepsis, rheumatoid arthritis and many others; including
CC application to indwelling devices) and thrombolytic disease, but also to
CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC immuno-modulators for treating multiple scierosis. (A) are administered
CC orally, topically, by injection or inhalation at 0.01-10 (preferably
CC 0.1-10) mg/kg/day.

SQ Sequence 1930 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
    for diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc Claim 1; fig. 1; 191pp; English.
This is full-length CRI protein, and shortened forms are new, lacking
                                                                                                                                         Ol-APR-1988; US-176532.
(TCEL) T Cell Sciences Inc; (UYJO) The Johns Hopkins University; (BRIG*) The Brigham and Women's Hospital.
Fearon DT, Kilokstein LB, Wong W, Carson G, Concino MF, Makrides WPI; 89-309498/42.
                                                                                              New nucleic acid sequences
                                                                                                                  N-PSDB; N91477
                                                                                                                                                                                                                                              05-OCT-1989.
31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                        CR1 protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P92219 standard; protein; 2317 AA. P92219;
                                                                                                                                                                                                                                                                                              WO8909220-A.
                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                   Complement; cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 PTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.18;
Local Similarity 31.48;
es 97; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRCTLKPCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                         10. .50
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                          encoding new CR1 protein - and its fragment
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Pred. No. 3.96e-31;
66; Mismatches 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 36;
                                                                                                                                                         SC;
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region.

The proteins and fragments bind C3b and/or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                  18-APR-1991.
25-SEP-1990; U05454.
26-SEP-1998; US-412745.
26-SEP-1990; US-912349.
(TCEL-) T CELL SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x-untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homoLogous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and -C can detect CR2 sequences. They are useful in diagnosing and treating immune disorders, and prevent
                                                                                                                                                                                                                                                                                                                                                                                                                               Partial human complement type 1 receptor. complement system; C3b/C4b receptor; CR1; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      perfusion injury
                          (UYJO ) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
FEBRION DT, Klickstein LB, Wong WW, Ca
Makrides SC, Marsh HC;
WPI: 91-132854/18.
                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R11982 standard; Protein; 1537 AA.
                                                                                                                                                                                                                                                                                                                                          region
                  N-PSDB; Q11643
                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                 region
                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                     immune response; long homologous repeat; LHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
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 complement receptor type 1 gene,
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llarity 31.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                      1521..1526
/note= "has 67 per cent homology to
kinase C phosphorylation in the EGF
receptor"
                                                                                                                                                                                                                                                     1495. .1498
/note= "positively-charged; preceded sequence"
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                  'label=
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                                                                                                                                                                                                                                                                                                  LHR-D
                                                                                                                                                                                                                                                                                                                            LHR-C
                                                                                                                                                                                                                                                                                                                                                             LHR-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 409; DB 1;
Pred. No. 3.96e-31;
66; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 110; Indels 36;
                                                            Carson
   encoded proteins and
                                                            GR,
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ID ACCOMPAND PRACTION OF THE PRACTICAL PRACTIC
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Best Local Similarity 28.8%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence comprises three of the four tandem, direct, long homologous repeats of the full-length F allozyme of CRL LHR-A is absent. Each LHR might represent a single C3b/C4b binding domain, making the receptor multivalent. The LHR's are composed of 7 short consensus repeats of 60-70 residues resembling the SCR's of other C3/C4 binding proteins. The protein and fragments of it having C3L and/or C4b binding activity can be used to treat immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragments - for treatment of immune disorders, myocardial infarct, damage due to inflammmation and in treatment of thrombosis Disclosure; Fig 5; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also Q11642.
Sequence 1537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or disorders involving inappropriate complement activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1202 PRCTVKSCD 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1085 STNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPGFVMVGSHTVQCQTNGRWGPKLPHC 1144
                        Human complement receptor type 1 gene, encoded proteins and fragments - for treatment of immune disorders, myocardial idamage due to inflammmation and in treatment of thrombosis Claim 41; Fig 1; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human complement type 1 receptor; complement system; C3b/C4b receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 969
                                                                                                                                                                                                                       (TCELL) T CELL SCI INC.
(UVJO) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
FEATON DT, Klickstein LB, Wong WW, Ca
Makrides SC, Marsh HC;
                                                                                                                                                                                                                                                                                                                                                                                          18-APR-1991.
25-SEP-1990; U05454.
26-SEP-1989; US-412745.
26-SEP-1990; US-912349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R11810 standard; Protein; 2039
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                                                                                                                                                                   N-PSDB; Q11642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response; clone lambda T109.1.
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The invention also covers fragments of this protein which have the
                                                                                                                                                                                                  WPI; 91-132854/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 PRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-RVCQPPPEILHGEHTLSHQDNFSPGQEVFYSCEPS-Y-DLRGAASLHCTPQGDWSPEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYSNNR-TS--FHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCI 1084
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42. .2039
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                                                                                                                                                                                                                                                                    Carson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR1; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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Best Local S
Matches 8
for diagnosis etc.

Claim 11; Fig 2 and R11810; 23pp; English.

The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

168:1255-1270. It encodes the first 8 and a half amino terminal

SCRs of CR1. The invention concerns analogues of "regulator of
                                                                                                                                28-APR-1992; 303826.
03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON.
Atkinson JP, Hourcade D, Krych M;
                                                                                 treating auto:immune diseases,
                                                                                            Complement activity regulator protein analogues - useful for
                                                                                                                       WPI; 92-375009/46
                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1993 (first entry)
CR1-4 (85R, 87N) analogue.
Short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                     EP-512733-A.
                                                                                                                                                                                                                                                                                                                                    region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ability to bind C3b and/or C4b, have cofactor I activity or can inhibit C3 or C5 convertase activity. The full-length protein, or its specified fragments are used to treat patients with immune disorders or a disorder caused by inappropriate complement activity. The protein is also used to treat thrombotic conditions in humans and animals. See also Q11643.
                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R28553 standard; peptide; 543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1471 NTDT-QFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGD 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 PRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-RVCQPPPEILHGEHTLSHQDNFSPGQEVFYSCEPS-Y-DLRGAASLHCTPQGDWSPEA 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEKSCDNP-YIPNGDYS-PLRIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIP-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPGFVMVGSHTVQCQTNGRWGPKLPHC 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYSNNR-TS--FHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCI 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGNVFEYGVKAVYTCNEGYQLLGE--INYRECDTD-GWTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 16.0%;
Similarity 28.8%;
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85
                                                                                                                                                                                                                                                  /note= ^{\text{m}}Gln substituted by Arg (SCR-9)^{\text{m}}
                                                                                                                                                                                                                              /note= "Lys substituted by Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  label= SCR-2
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                                                                                 to suppress transplant
                                                                                 rejection,
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Best Local
Complement activity regulator protein analogues - useful for
treating auto:immune diseases, to suppress transplant reject:
for diagnosis etc.
Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                  Atkinson JP, Hourcade D, WPI; 92-375009/46.
                                                                                                                                                                                                                     28-APR-1992; 303826.
03-MAY-1991; US-6955
                                                                                                                                                                                            03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                     EP-512733-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR 1993 (first entry)
CR1-4 (99H, 103E) analogue.
Short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type I receptor.
                                                                                                                                                                                                                                                                                     11-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                 misc_difference 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R28557 standard; peptide; 543 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-I-QFGSRINYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
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Similarity 31.1%;
96; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                        /note= "Thr substituted by Glu (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SCR-2
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                                                                                                                                                               Krych M;
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67; Mismatches 110; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 404; DB 1;
Pred. No. 1.36e-30;
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                                                               rejection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEQ from the full-length CR1 amino acid sequence having GENESEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accession number R11810 and descriptions in the disclosure.
                                                       11-NOV-1992.
28-APR-1992; 303826.
23-MAY-1991; US-699514.
33-MAY-1991; US-699514.
(UNIW ) UNIV WASHINGTON.
Atkinson JP, Hourcade D, Krych M; WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                CRI-4 (1145) analogue.
short consensus repeat; regulator of complement activation;
c3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R28560 standard; peptide; 543 AA.
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                    Complement activity regulator protein analogues - useful treating auto:immune diseases, to suppress transplant rej
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 -PRCTLKPCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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  diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CS-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEEKSCONP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG--WTNDIPICEVVKC-LPVTAPENG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-I-QFGSQIKYSCTKGYRLIGHSS-AECIISGDTVIWDNETPICDRIPCGLPPTIT-NG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
      etc.
                                                                                                                                                                                                                                                                  451...510
/label= SCR-8
511...543
                                                                                                                                                                                                                 /label= SCR-9
/note= "TRUNCATED"
114
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                               /note= "Asp substituted
                                                                                                                                                                                                                                                                                                                                  'label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                      'label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%;
                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 403; DB 1;
Pred. No. 1.74e-30;
67; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 108; Indels
                                                                                                                                                                                               by Ser (SCR-9)"
                          transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEO accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 2 and R11810; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                     CR1-4 (64K) analogue.

Short consensus repeat; regulator of complement activation; consensus repeat; human complement type 1 receptor.
                             (UNIW ) UNIV WASHINGTON. Atkinson JP, Hourcade D, WPI; 92-375009/46.
                                                                           11-NOV-1992.
28-APR-1992; 303826.
03-MAY-1991; US-695514
                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                                                            R28550;
19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                           R28550 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                             region
Complement activity regulator protein analogues - useful treating auto:immune diseases, to suppress transplant rej
                                                                                                                                                              misc_difference
                                                                                                                                                                                                             region
                                                                                                                                                                                                                                            region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%;
Local Similarity 31.1%;
hes 96; Conservation
                                                                                                                               EP-512733-A.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWSNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIS-CKSPDVINGSPISQ-KIIYKENERPQYKCNMGYEYSERGDAVCTE-@GWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                         /note= "TRUNCATED" 64
                                                                                                                                                                                                                                               451.
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                               /label= SCR-2
451. .510
                                                                                                                                               /note= "Arg substituted
                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                            'label = SCR-1
                                                                                                                                                                                                                                                                                .122
                                                                                                                                                                                                               .543
                                                                                                                                                                                                                              SCR-8
                                                  Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 402; DB 1;
Pred. No. 2.22e-30;
67; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 110;
                                                                                                                                                by
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        rejection
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Claim 11; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; R11810; English.

Claim 13; Fig 2 and R11810; English.

Claim 14; Fig 2 and R11810; English.

Claim 15; Fig 2 and R11810; English.

Claim 16; Fig 2 and R11810; English.

Claim 17; Fig 2 and R11810; English.

Claim 18; Fig 2 and R11810; English.
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Best Local Similarity
                                                                                  11-NOV-1992.
28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R28552 standard; peptide; 543 AA.
R28552;
19-MAR-1993 (first entry)
CRI-4 (78T, 79D) analogue.
Short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
    (UNIW ) UNIV
Atkinson JP,
                                                                                                                                                                                                      EP-512733-A.
                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                                                                   misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 IVSSAMEPDREYHFGQAVRFYCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 PTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCKNPPDPVNGMVHVIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
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                                                                                  303826.
US-695514.
WASHINGTON.
Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%;
larity 31.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                      /note= "Gly substituted by Asp (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                /label= SCR-9
/note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451. .510
/label= SCR-8
                                                                                                                                                                                                                                                                                                             note= "Lys substituted by Thr (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SCR-1
61. .122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 111; Indels 36;
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If for diagnosis etc.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Chaim 12; Fig 2 and R11810; English.

Chaim 12; Fig 2 and R1810; English 2 and a half amino terminal 2 complement activation, proteins or truncated, hybrid or recombinant 2 complement activation variants of it are claimed in which certain 2 specified substitution variants of it are claimed in which certain 2 complement activation of it are claimed in which certain 3 constitutes in SCR-2 which have been identified as important for the 2 contain the CR1-4 sequence; the specification does not 2 contain the CR1-4 sequence the sequence have was constructed 2 contain the CR1-4 sequence the sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                310 PTCEVKSCD
                                                                                 245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                  189 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                              193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                              139 IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                         136 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                          83 GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                        78 TDI-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPD-PVNGMYHVI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 15.7%;
Local Similarity 30.7%;
es 95; Conservative
                                                                                                                             S-RVCQPPPDVLHAERTQRDKDNESPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
PRCTLKPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AA;
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 399; DB 1;
Pred. No. 4.65e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
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Search completed: Thu Jun 8 21:45:07 2000 Job time: 16 secs.

^;<u>~</u>

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jun 8 21:45:24 2000; MasPar time 19.71 Seconds 787.259 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence:

>US-09-316-163-11 (1-329) from US09316163.pep 2539 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 34

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Lighting first 45 summaries

Database: pir62 (1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 43.995; Variance 69.824; scale 0.630

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	ر د د	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	σ	4	ω	N	1	Result
362	371	373	376	387	388	388	402	403	404	409	409	423	433	433	438	447	603	1236	1772	2539	2539	Score
14.3	14.5	14.7	14.8	15.2	15.3	15.3		15.9	15.9	16.1	16.1	16.7	17.1	17.1	17.3	17.6	23.7	48.7	69.8	100.0	100.0	Query Match 1
579	768 768	676	830	482	560	263	469	661	558	2489	2039	2014	597	303	452	597	1053	669	1234	1231	449	Length 1
21	√	۷ ^د	N	N	N		Н	N	N	ν	N	N	ш	N	N	Ь	N	N	ш	ш	ш	DB
A56740	153821	A45900	A30359	A34924	T16833	WMVZSP	NBMSC4	I36937	S57953	173012	A28507	I36936	NBHUC4	H35068	A35068	S53711	S46199	S65551	HSMEN	NBHUH	NBHUHS	ID
re	P-selectin - rat		P-selectin precursor	complement C3b/C4b re	hypothetical protein	apolipoprotein H nomo	C4b-binding protein a		C4BP protein alpha ch	complement C3b/C4b re	complement C3b/C4b re	complement receptor 1	C4b-binding protein a	-	complement factor H-r	C4BP alpha chain prec	O		nt factor F	Ξ	complement factor H p	Description
3.33e-59	. 05e-	2.20e-61	1.336-02	2.846-65	1.62e-65	1.020-00	6.13e-69		1.98e-69	1.18e-70	1.18e-/0	4.250-74	1.45e+/6	ı ~	1 ~	5.01e-80	2.98e-119	3./1e-284	0.000+00	0.00e+00	0.00e+00	Pred. No.

44	44	43	42	41	40	39	38	37	36	ა წ	34	33	32	31	30	29	28	27	26	25	24	
309	314	318	320	325	328	328	331	336	335	ა 35	334	338	338	340	341	341	343	357	357	360	363	
12.2	12.4	12.5			12.9		13.0	13.2	13.2	13.2	13.2	13.3	13.3	13.4	13.4	13.4	13.5	14.1	14.1	14.2	14.3	
551	612	610	610	1091	369	362	345	497	384	377	345	369	349	661	360	302	768	610	263	808	668	
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146709	S23174	A32606	A35046	PL0009	JC5138	JC5194	NBHU	JC2054	S01896	I54479	NBBO	157998	G02913	KFHU13	WMBE2E	WMBE1E	A42755	I46001	C36838	D35069	A46013	
-	endothelial leukocyte	endothelial leukocyte		C	membrane colactor pro			complement regulatory		pro	rec	pro	(H	actor X1	ie			בם	, ř	Iactor H-I	n factor XI	
1.58e-46	1.04e-4/	1.1/6-40	3.91e-49	2.036-30	4.0/6-01	4.8/6-51	9.3/e-52	. 986-0	י ה	יסי	1.808-52	1.996-00	1.996-53	1 000 53	0.79E-U4	3./9E-04	1.208-04	1 0 C C C		E 070-50	1.91e-59	

#title Human pa: col #cross-references #accession A278' #molecule_type #residues ##note	#accession ##status ##status ##molecule_ ##residues ##note REFERENCE #authors #journal	##CLESSION ##MOLECULE_Type mRNA ##residues 1-44 ##cross-references E ##cross-references P ##note part ##note A60238 #authors Estaller, #journal Human com #title from al #cross-references MUID:	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title #cross-reference
an complement factor artial cDNA sequence ontaining the bindin MUID: 87054207 377 a mRNA arti, 55-401, 'Y', 40 an additional nucl Glu-310 was thou ignored in trans	with conc ##label E s of this waeble, W. (1986) 16:	##molecule_type mRNA ##residues 1-40 ##label RIP ##coss-references EMBL:X07523; EMBL:Y00716; NID:g32492; ##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492; ##note part of this sequence, including the amino end of the mature protein was confirmed by protein sequencing ##note A02-Tyr was also found ##note A60238 ##note Afordaler, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. journal Eur. J. Immunol. (1991) 21:799-802 title from alternatively spliced transcripts. cross-references MUID:91184292	JIT 1 NBHUHS #type complete RY Complement factor H precursor, short splice form - human complement factor H-related protein; complement protein H #formal_name Homo sapiens #common_name man 31-Dec-1993 #sequence_revision 23-Feb-1996 #text_change ESSIONS S030.13; B60238; A27877; A61103; A26505; S10479 ERENCE #title Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B. #journal Biochem. J. (1998) 249:593-602 #tross-references MUID:88134059 *coossion S03013 **Coossion S03013*** **Coossion S03013** **Coossi

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FEATURE
                                                                                                                                                                                                                CLASSIFICATION
                                                                                                                                                                      KEYWORDS
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#map_position 1q32-1q32 
GENETICS HF2
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                                                                      19-449
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#map_position 1q32-1q32
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#journal Eur. J. Immunol. (1987) 17:1485-1489
#title truncated gene product of 43 kDa in human liver.
#cross-references_MUID:88055295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #contents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
##residues 226-01,'Y',403-449 ##label KRI
##cross-references GB:M12383; NID:9180472; PIDN:AAA52013.1; PID:9180473
##cross-references GB:M12383; NID:9180472; PIDN:AAA52013.1; PID:9180473
WT Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
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##molecule_type mRNA
27-76 ##label SC2
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in liver. See also PIR:NBHUH
                                                                                                                                                                                                                                                                                                                   a cofactor in the inactivation of C3b by serine proteinase I;
                                                                                                                                                 alternative splicing; complement alternate pathway;
                                                                                                                                                                                              #superfamily complement factor H; complement factor H repeat
                                                                                                                                                                                                                                                                                                                                                                                                                      the correspondence between the two loci and the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kristensen, T.; Wetsel, R.A.; Tack, B.F.
J. Immunol. (1986) 136:3407-3411
Structural analysis of human complement protein H: homology with C4b binding protein, beta(2)-glycoprotein I, and the Ba fragment of B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A26505
Sim, R.B.; Discipio, R.G.
Biochem. J. (1982) 205:285-293
Purification and structural studies on the complement-system control protein beta-1-H (factor H).
                                                                                                                                                                                                                               complement alternate pathway
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Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
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                                                                                                                                    glycoprotein;
                                                                                                                                                                                                                                             also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway
                                                                                                                                                                                                                                                                                                                                                                               indicated is unclear; factor {\tt H} has been reported several allelic forms
#domain complement factor H repeat homology #label FH01\
                       *product complement factor H, short splice form *status experimental *label MAT \
                                                                        #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     this is a partial sequence of an alternatively spliced 1.8 kilobase mRNA that is translated to yield a 43 K
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                                    #title
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                                                                                                                                                                                                                                                                                                                                                #journal
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178-205,210-251,
237-262,267-309,
294-320,325-374,
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357-385,389-431,
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                                                                                                              ##rote parts of the mature protein, were confirmed by protein
                                                                                                                                                                                                                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 RCTLKPCDYPDIKHGGLYHENMRRPYFPV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LPSCEEKSCDNPYTPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 LPSCEEKSCDNPYIPNGDYSPLRIKHRIGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SKEKPKCVETSCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PICEVVKCLPYTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 SKEKPKCVEISCKSPDVINGSPISQKIIYKENERPQYKCNMGYEYSERGDAVCTESGWRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
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Local Similarity 100.0%;
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                 Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived
                                                                                                                                                                                                                                                                                                           The complete amino acid sequence of human complement factor
                                                                                                                                                                                                                                                                                                                                   Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B. Biochem. J. (1988) 249:593-602
                                                                                                                                                                                                                                                                                                                                                                                                                                  NBHUH #type complete complement factor H precursor, long splice form - human formal_name Homo sapiens #common_name man 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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from alternatively spliced transcripts
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complement factor H repeat homology #label FH03\
complement factor H repeat homology #label FH04\
cell attachment (R-G-D) motif\
complement factor H repeat homology #label FH05\
complement factor H repeat homology #label FH06\
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#journal Biosci. Rep. (1987) 7:201-207
#title Sequence analysis of a cDNA clone encoding the C-terminal end of human complement factor H.
#cross-references MUID:88025472
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#journal Blosci. Rep. (1986) 6:65-72
Partial characterization of human complement factor H by protein and cDNA sequencing: homology with other complement and non-complement proteins.
#cross-references MUID:86188123
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#accession A60238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;
#journal Biochemistry (1992) 31:3626-3634
#title Example of the complement control protein module.
#cross-references MUID:92232649
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#journal Biochem. J. (1982) 205:285-293
#title Purification and structural studies on the complement-system
control protein beta-1-H (factor H).
#cross-references MUID:83048213
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##cross-references GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
##note parts of this sequence were determined by protein
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##residues 19-20,'Q',22-29,'V',31-33,'Q',35 ##label SIM
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                                               ##cross-references GB:M65294; NID:g183766; PIDN:AAA35948.1; PID:g183767
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                                                                                                                                                                                                           J. Immunol. (1991) 146:3190-3196
Cloning of the 1.4-kb mRNA species of human complement factor
H reveals a novel member of the short consensus repeat
family related to the carboxy terminal of the classical
150-kDa molecule.
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J. Mol. Biol. (1991) 219:717-725
Three-dimensional structure of a complement control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; Campbell, I.D.
Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano
                                                                                                                                                                                                                                                                                                                                           Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.; Weiss, E.H.
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416-442,448-494, 477-505,509-553, 536-564,569-611, 597-623,630-673, 659-684,691-733,

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##residues 411-419;574-578,580-582 ##label CAR
#Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
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Biochim. Biophys. Acta (1996) 1289:305-311
Factor H co-purifies with thrombospondin isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a cofactor in the inactivation of C3b by serine proteinase I;
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781-803,811-853,
839-864,870-915,
901-926,931-973,
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329;
Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y. J. Immunol. (1990) 144:358-362

Demonstration of an unusual allelic variation of mouse factor H by the complete cDNA sequence of the H.2 allotype.
                                                                                                                                                                                       Kristensen, T.; Tack, B.F.
Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967
Murine protein H is comprised of 20 repeating units, 61 amino acids in length.
                                                                                                                                                                                                                                                                                                                  protein beta-1-H

#formal_name Mus musculus #common_name house mouse
30.Sep-1987 #sequence_revision 30-Sep-1987 #text_change
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536-564,569-610,

597-622,629-672,

658-682,690-732,

658-683,690-732,

718-743,752-791,

780-802,808-850,

836-861,867-920,
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21-66,52-80,85-129,
114-141,146-192,
178-205,210-251,
237-262,267-309,
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357-385,389-431,
416-442,448-494,
477-505,509-553,
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1053-1107
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569-622
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Biochemistry (1989) 28:9891-9897
Analysis of complement factor H mRNA expression:
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Db 7 LAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPENGKI 66
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296-349
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#journal Biochem. J. (1996) 315:523-531
#title Prediction from sequence comparisons of residues of factor H
#title involved in the interaction with complement component C3b.
#cross-references_MUID:96202005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNEKPRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGDAVCTGSGWSS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCTLKPCEFPQFKYGRLYYEESLRPNFPV 347
                               h 48.7%;
Similarity 61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *superfamily complement factor H; complement factor H repeat
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                                                                                                                                      #length 669
       Conservative
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                                                                                                                                                                  #domain complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-669 ##label SOA
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                                                                                                                                      #checksum 8335
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Pred. No. 0.00e+00;
49; Mismatches 64; Indels
       score 1236; DB 2; |
Pred. No. 3.71e-284;
35; Mismatches 59;
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                                                                   Length 669;
       Indels
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Best Local Similarity 34.1%;
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#title
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935-989
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682-738
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334-389
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#accession $46199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 RPELSKYRGQDKITYECKKGFFPEIRGTDATCTRDGWVPVPRCAWKPCSYPVIKHGRLYY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 SPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGLYH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-1053 ##label DAH1
##cross-references EMBL:L21703; NID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
  141
                                   162 IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type protein
##residues 526-532,'X',534-537;809-817,'X',819-826 ##label DAH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
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                                                                                 81
                                                                                                                                                                                                       47 EASYPGGROVRVGCNVGY-S-GFFKLVCVEGKWETRGA--KCOPRSCGHPGDAQFADFHL 102
                                                                                                                                                                  21
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SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                        AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQV 161
                                                                                 TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV 140
                                                                                                                                                                                                                                                   101;
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Blochem. J. (1994) 301:391-397
Cloning and characterization of a cDNA representing a
putative complement regulatory plasma protein from barred
sand bass (Parablax neblifer).
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19_Mar-1997_#sequence_revision 06-Jun-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                    #molecular-weight 117597
                                                                                                                                                                                                                                                     49; Mismatches 129;
                                                                                                                                                                                                                                                                       Score 603; DB 2; I
Pred. No. 2.98e-119;
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112-169
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                                                                                                     299
                                                                                                                                       357 FAGCEAICCPHPQLDNGAI-TEHSRNP 382
                                                                                                                                                                                                                                                                                                                                                                                   180 IINGK-HNGGNE-DIH-TYGSSVTYSCNPRFSLLGEASISCTVKNKTVGVWSPSPPVCKE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                 78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references EMBL: Z35490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 SENEYQTGTILKYTCRPGYTRNGLNPILTCKPRGLW-SYDTF--CVKKRCRNPGDLPNGQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
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                                                                                                                                                                         KSC-DNPYIPNG--D-YS-PLRIK-HRTGDEITYQCRNGFYPATRGNT-AKCTST-GWIP 298
                                                                                                                                                                                                                                                                                                     IICSPPNVPHGKIISGFGPIYNYKDSIMYTCIDGFVLRGSSLIHCELDSKWNPSPPVCES 296
                                                                                            APRCTLKPCDYPDIKHGGLYHENMRRP 325
                                                                                                                                                                                                                 NSCLGLPNVPHASQQGYQWSTKEGVYSVGTELRYKCRPGYRPVADEPIIVTCQEDLRWSP 356
                                                                                                                                                                                                                                                                                                                                               PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVE 189
                                                                                                                                                                                                                                                            ISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCT-ESGWRPLPS-CEE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEVKT-D-FSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVEWSDPLPKCEIVKCEPPPN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDQTYPEGTQAIYKCRPGYRSLG-NVIMVCR-KGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPISQKIIYKENERFQYKCNMGYEYSERGDA-V--CTESGWRPLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNVPGAIREYKENDVLHYECDRAFKHIDRPSTCIKQGIKAEWSPTPLCESIKCRLTIMDG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.6%;
Similarity 30.9%;
               A35068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de Frutos, P.G.; Dahlbaeck, B.
Biochim. Biophys. Acta (1995) 1261:285-289
cDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein
modules which bind C4b.
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C4BP alpha chain precursor - rabbit
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         #type fragment
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Pred. No. 5.01e-80;
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B.F.; Chaplin, D.D.
#journal J. Biol. Chem. (1990) 265:3193-3201
#title Identification and sequence analysis of four complement
factor H-related transcripts in mouse liver.
#cross-references MUID:90153969
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                                                                                                                                                                                       ##residues 1.303 ##label VIK
##cross-references GB:M29007; NID:g192557; PID:g309164; GB:J05259
##note translation of the nucleotide sequence is not complete
#FICATION #superfamily complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
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Local Similarity 56.4%;
               #length 303
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apollipoprotein H-related protein 23L1 - mouse
#formal_name Mus musculis #common_name house mouse
27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change
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B.F.; Chaplin, D.D.
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#domain complement factor H repeat homology #label FH01\
#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04
#th 303 #molecular-weight 34498 #checksum 2835
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Pred. No. 8.46e-78;
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FH5/
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17.1%;

Score 433; DB 2;

Length 303;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y.
#journal Biochem. Biophys. Res. Commun. (1989) 165:138-144
Molecular cloning of the cDNA coding for proline-rich protein
(PRP): identity of PRP as C4b-binding protein.
#cross-references_MUID:90073699
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Blochem. J. (1985) 230:133-141
Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.
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FEBS Lett. (1988) 232:328-332
Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of
the C4bp cDNA sequence.
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13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change
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Rodriguez de Cordoba, S.; Sanchez-Corral, P.; Rey-Campos, J. J. Exp. Med. (1991) 173:1073-1082
Structure of the gene coding for the alpha polypeptide chain of the human complement component C4b-binding protein.
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17; Mismatches 25;
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##cross-references GB:M62486; NID:g1904840; pIDN:AA36506.1; pID:g190500
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#title Binding site for vitamin K-dependent protein S on complement case-references MUID:89034204
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#title Genomic organization of the alpha chain of the human
#cross-references MUID:91113199
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N-terminal sequence analysis and alignment of the fragment
produced by limited proteolysis with chymotrypsin and the
peptides produced by cyanogen bromide treatment.
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The region Ser(333)-Arg(356) of the alpha-chain of human
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Mol. Immunol. (1985) 22:427-435
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                          Primary sequence of an alternatively spliced form of CRI.
Candidate for the 75,000 M(r) complement receptor expressed
on chimpanzee erythrocytes.

Oces MUID:94292799
                                                                                                                             Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.;
                                                                                                                                                                                                  I36936 #type fragment
complement receptor 1 - chimpanzee (fragment)
fformal_name Pan troglodytes #common_name chimpanzee
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                I36936
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                                                                                         Atkinson, J.P.
Immunol. (1994) 153:691-700
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Pred. No. 1.45e-76;
68; Mismatches 132;
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#cross-references MUID:89035992
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1622 S-RYCQPPPEILHGEHTPSHQDNFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWSPEA 1678
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                                                                                                                                                                A28507 #type complete complement C3b/C4b receptor precursor, membrane-bound (allotype F) - human complement receptor type 1 (CR1); surface glycoprotein CD35
Smith, J.A.; Fearon, D.T.

J. Exp. Med. (1988) 168:1699-1717

Identification of distinct C3b and C4b recognition sites the human C3b/C4b receptor (CR1, CD35) by deletion
                                                     Klickstein, L.B.; Bartow, T.J.; Miletic, V.; Rabson, L.D.;
Smith, J.A.; Fearon, D.T.
                                                                                                     S03843; A28507; I56203; A24748; B24748; C24748
                                                                                                                           19-Nov-1988 #sequence_revision 06-Sep-1996 #text_change
10-Sep-1997
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Pred. No. 4.26e-74;
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493-549
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104-161
166-232
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#map_position 1q32-1q32
41/1; 101/1; 134/2; 163/1; 296/1; 355/1; 389/2; 418/1; 491/1;
#introns 451/1; 584/2; 613/1; 746/1; 805/1; 839/2; 868/1; 941/1;
1001/1; 1034/2; 1063/1; 1196/1; 1255/1; 1289/2; 1318/1;
1394/1; 1454/1; 1487/2; 1516/1; 1649/1; 1708/1; 1742/2;
1771/1; 1847/1; 1906/1; 1968/1; 1976/1; 2001/2; 2036/2
ASSIFICATION #superfamily complement factor H repeat homology
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1828-1849,'D',1851-1875,'I',1877-2039  ##label RES

**cross-references GB:L17418; NID:g306678; PID:g306680

NCE A94073
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J. Exp. Med. (1987) 165:1095-1112

Human C3b/C4b receptor (CR1). Demonstration of long homologous repeating domains that are composed of consensus repeats characteristic of C3/C4 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wong, W.W.; Klickstein, L.B.; Smith, J.A.; Weis, J.H.; Fearon, D.T.

Fearon, D.T.

Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7711-7715

Identification of a partial cDNA clone for the human receptor for complement fragments C3b/C4b.
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J. Immunol. (1993) 151:6214-6224

Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S
                                                                                                                                                                                                                                                                                                                                                                                                      duplication; glycoprotein; transmembrane protein
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1774-1840
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                                     #cross-references_MUID:89176869
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##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
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Similarity 31.4%;
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J. Immunol. (1993) 151:6214-6224
Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173012 #type complete
complement C3b/C4b receptor (allotype S) precursor - human
complement receptor type 1 (CR1); surface glycoprotein CD3'
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                         Wong, W.W.; Cahill, J.M.; Rosen, M.D.; Kennedy, C.A.; Bonaccio, E.T.; Morris, M.J.; Wilson, J.G.; Klicksteir L.B.; Fearon, D.T.
J. Exp. Med. (1989) 169:847-863
Structure of the human CRI gene. Molecular basis of the structural and quantitative polymorphisms and identification of a new CRI-like allele.
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66; Mismatches 110
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                                                                                                                                                                M.D.; Kennedy, C.A.;
Wilson, J.G.; Klickstein,
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##cross-references EMBL:X14362; NI
##experimental_source clone CR1-4
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y Match 16.1%;
Local Similarity 31.4%;
hes 97; Conservative
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Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1.
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                                        155 EEF-FTYRSSVTYKCDPDFTLLGNASITCTVVNKTVGVWSPSPPTCERIICPWPKVLHGT 213
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                                                                                 90 VKAVYTCNEGYQLLGE-INYRECDTDG--WTNDIPICEVVKC-LPVTAPENGKIVSSAME 145
                                                                                                                                                                  32 YKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYG
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#formal_name Rattus norvegicus #common_name Norway rat
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*title Primary sequence of an alternatively spliced form of CR1.

Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes.

*cross-references MUID:94292799

*accession 136937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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396-462
531-587
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213-268
272-328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 INSGFKHTYKYKDSVRFVCQKGFVLRGSGVIHCEADGSWSPVPVCELNSCTDIPDIPNAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 IKHGGLYHENMRRP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 PKSVRVIQHEKAHP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-661 ##label RES
##cross-references GB:L24921; NID:g557726; PID:g557727
FICATION #superfamily complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
                                                                                                                                                                                                                               139 IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                      152 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 208
    300 PRCTLKPCD 308
                                        326 PTCEVKSCD 334
                                                                         245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA- 299
                                                                                                               269 S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASLRCTPQGDWSPAT 325
                                                                                                                                                                                        209 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPPRVKCQALNKWEPELPSC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 15.9%;
Local Similarity 31.1%;
hes 96; Conservative
                                                                                                                                                                                                                                                                                                          83 GNVFEYGVKAVYTCNEGYOLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                      24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                          38 FPIGTYLNYECRPGYYGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPD-PVNGMVHVI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y--SP-LRIKH--RTGDEITYQCRNGFYPATRGN-TAKC-TSTGWIPAPRCTLKPCDYPD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LITSPRPRKEDVYPVGTVLRYICRPGYEPATRQPMTVICQKDLSWSMLRGCKEICCPVPD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRPLPSCEEKSC-DNPYIPNGD 258
                                                                                                                                                        EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                 KDI-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement receptor 1 - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-Jul-1999
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#domain complement factor H repeat homology
#domain complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #type fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.49e-69;
66; Mismatches 111; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 403; DB 2;
Pred. No. 3.49e-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
homology
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FH07\
FH08
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FH02/
FH03/
FH04/
FH05/
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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120-176
181-240
245-299
303-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #cross-references MUID:88024997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                         117 KKHCRNPGYLDNG-Y-VNGETI-TFGSQIEFSCQEGFILVGSST-SSCEVRGKGVAWSNP 172
345 FSKWKGTAPQCKA-LCQKPEVGNGTLSDEK 373
                                            235 ESG-WRPLPSCEEKSCD-NPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCT 292
                                                                                      289 GNGNWSSLPTCEF-DCDLPPAIVNGYYTSM-VYSKIT-LYTYECDKGYRLVGKAIIS-CS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 PPPAIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMYYCKPSGEW-EIS-VS-CA 116
                                                                                                                                                                                                                                                                                                                            64 KRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTND 119
                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 15.8%;
Local Similarity 27.9%;
es 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4BP controls the classical pathway of complement activation. It binds as a cofactor to C3b/C4b inactivation (C3bINA), which then hydrolyzes the complement fragment C4b. It also accelerates the degradation of the C4bC2a complex (C3 convertase) by dissociating the complement fragment C2a.
                                                                                                                                                                                                                                 IPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD 177
                                                                                                                                                                                                                                                                             FPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLVGSPFIGCTVVNK 228
                                                                                                                                                                                                                                                                                                                                                                                                                        PPRRNTEILTGSWSDQT-YPEGTQAIYKCRPGY-RSLGNVIMVCR-KGEWVALNPLRKCQ 63
                                                                                                                                     GF--WSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCT 234
                                                                                                                                                                                  TYPYWSSSPPTCEKIICSQPNILHGYIYSGYKATYTHRDSVRLACLNGTYLRGRHYIECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In mouse, C4BP is a multimeric protein of noncovalently associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry (1987) 26:4668-4674 cDNA structure of murine C4b-binding protein, a regulatory component of the serum complement system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name Mus musculus #common_name house mouse 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4B-) proline rich protein C4BP; proline rich protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acute phase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily C4b-binding protein alpha chain; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kristensen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #length 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycoprotein; plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor H repeat homology
ute phase; chylomicron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the authors translated the codon GCT for residue 25 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH5\
#domain complement factor H repeat homology #label FH5\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #product C4b-binding protein alpha chain #status
predicted #label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.; Ogata, R.T.; Chung, L.P.; Reid, K.B.M.; Tack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #molecular-weight 51523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 402; DB 1; Let pred. No. 6.13e-69; 74; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement pathway; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 469;
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Qy 293 STGWI-PAPRCTLKPCDYPDIKHGGLYHEN 321

Search completed: Thu Jun 8 21:45:47 2000 Job time: 23 secs.

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Tabular output not generated. MPsrch_pp ***************************** Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Thu Jun 8 21:46:04 2000; MasPar time 12.45 Seconds 804.485 Million cell updates/sec >US-09-316-163-11 (1-329) from US09316163.pep 2539 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 329

Run on:

Description: Perfect Score:

Sequence:

Scoring table: PAM 150 Gap 11

Searched:

Post-processing: Min.Mnum Match 0% Lighting first 45 summaries

83857 seqs, 30454973 residues

Database: swiss-prot38 1:swissprot

Statistics:

Mean 44.764; Variance 62.937; scale 0.711

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1	Result
2539 4732 409 409 4002 3882 371 377 357 357 357 357 357 357 357 357 357	Score
100.0 69.8 17.1 15.9 15.3 14.6 14.6 14.3 13.5 13.2 13.2 13.2 13.2 13.2 13.2 13.2 13.2	Query Match Length
1231 1232 1239 2039 263 263 345 660 660 660 661 345 345 612 345 612 345	
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44 44 45	37 38 40 41	ω ω ω ω α α 4 τι α	27 28 31 31	24 25
220 220 220 220	276 271 254 238 232	284 281 280 276 276	30 20 20 20 20 20 20 20 20 20 20 20 20 20	306 306
8.7 8.7 8.7	10.9 10.7 10.0 9.4	11.1 11.0 10.9	11.8 11.8 11.8 11.8	12.1 12.1
372 372 372 372	1019 646 390 407 372	340 331 507 297 485	1033 330 549 611 381 1025	551 769
рррг				μμ
LEM1_PANTR LEM1_MACMU LEM1_HUMAN	LFC_TACTR LEM3_BOVIN DAF1_MOUSE DAF2_MOUSE LEM1_RAT	CFHD_HUMAN DAF_CAVPO APOH_RAT LEM2_BOVIN	CR2_HUMAN CFH1_HUMAN LEM2_RAT LEM2_CANFA DAF_HUMAN CR2_MOUSE	LEM2_RABIT LEM3_SHEEP
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SEQUENCE OF 19-35. MEDIJINE; 83048213. Sim R.B., Discipio R.G.; "Purification and structural studies on the complement-system control "purification and structural studies on the complement-system control protein beta 1H (Factor H).";	SEQUENCE OF 1047-1231 FROM N.A. MEDLINE; 91201892. Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.; Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.; "Cloning of the 1.4-kb mRNA species of human complement factor H "Cloning of the 1.4-kb mRNA species of human complement factor H reveals a novel member of the short consensus repeat family related to the carboxy terminal of the classical 150-kDa molecule."; J. Immunol. 146:3190-3196(1991).	M N N N N N N N N N N N N N N N N N N N	UDENCE FROM N.A. SUB-LIVER; SUB-LIVER; LINE; 88134059. Chem. J. Day A.J., Har oche J., Day A.J., Har oche J. Day A.J., Har ochem. J. 249:593-602(1 UDENCE OF 53-445 FROM N ULINE; 87054207. ulz T.F., Schwaeble W. man complement factor quence of the 38-kDa tr C3b.";	GEAH_HUMAN STANDARD; PRT; 1231 AA. PO8603; 01-ANG-1988 (Rel. 08, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) 15-FEB-4000 (Rel. 39, Last annotation update) COMPLEMENT FACTOR H PRECURSOR. HEI OR HF OR CFH. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]

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EMBL; Y00716; CAA68704 1; -.
EMBL; X04697; CAB41739.1; ALT_FRAME.
EMBL; M65294; AAA35948.1; -.
PIR; S00254; NBHUH.
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PIR; S03013; S03013.
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J. Mol. Biol. 232:268-284(1993).

-i. FUNCTION: FACTOR I EUNCTIONS AS A COFACTOR IN THE INACTIVATION OF C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3B BY COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALIZENNATIVE COMPLEMENT PATHWAY.

-i. SIMILARITY: CONVAINS 20 SUSHI (SCR) REPEATS.

-i. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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structure; Polymorphism.
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P06979;
Ol-JAN-1988 (Rel. 06, Created)
Ol-JAN-1988 (Rel. 06, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1-H).
                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                               Munoz-Canoves P., Tack B.F., Vik U.F. Munoz-Canoves P., Tack B.F., Vik U.F. "Analysis of complement factor H mRNA IFN-gamma increase the level of H in Biochemistry 28:9891-9897(1989).
                                                                                       "Demonstration of an unusual allelic variation of mouse the complete cDNA sequence of the H.2 allotype.";
J. Immunol. 144:358-352(1990).
-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE TN
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LOT H mRNA expression: dexamethasone of H in L cells.";
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Plasma; Glycoprotein; Repeat; Sushi;

BY SIMILARITY. COMPLEMENT FACTOR H

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P04003;
                                                                                                                   Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.; "Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein."; Biochem. Biophys. Res. Commun. 165:138-144(1989).
  Lintin
              SEQUENCE OF 9-81 FROM N.A. MEDLINE; 88242821.
                                                      Aso T., Okamura S., Matsuguchi T., "Genomic organization of the alpha protein gene.";
                                                                                        MEDLINE;
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01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         QPFCEEKRCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTGWIPVP
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 S.J.,
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Similarity 65.7%;
                                             Biophys. Res. Commun.
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Lewin A.R., Reid K.B.M.;
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Pred. No. 0.00e+00;
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                                         174:222-227(1991).
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human C4b-binding
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VITAMIN K -dependent protein and its complexes with vitamin K -dependent protein and its complexes with Proc. Natl. Acad. Sci. U.S.A. 80:34461-3465(1983).

C -!- FUNCTION. C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT CALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C4B. IT CALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEX OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEX OF THE CABCA ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CHAIN BIND WITH SERUM AMYLOID P COMPONENT.

C -!- SUBUNIT: DISULFIDE-LINKED CONPLEX OF C4BP ALPHA CHAINS AND 1 BETA CHAINS OF ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE ALPHA CHAIN, A 530 KD HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KD COMPLEX OF 6 ALPHA CHAIN SAND 1 BETA CHAIN. THE CENTRAL BODY OF THE SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.

C -!- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOROTEIN R.

C -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.

This SWISS-DEOR OF THE STATE CHAIN AND TO PIG APOLIPOROTEIN R.
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, AND LIGAND
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"Molecular cloning and characterization of the cDNA coding binding protein, a regulatory protein of the classical path
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"Studies on the structure of the human C4b-binding protein gene.";
FEBS Lett. 204:77-81(1986).
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em. J. 230:133-141(1985).
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EMBL; M11617; AAA52298.1;
EMBL; M11618; AAA52299.1;
EMBL; Y00816; CAA68755.1;
EMBL; X05309; CAA28933.1;
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Homo sagines (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; metazoa; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human C3b/C4b receptor (CR1). Demonstration of long homologous repeating domains that are composed of the short consensus repeats characteristics of C3/C4 binding proteins.";
J. Exp. Med. 165:1095-1112(1987).
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"Identification of distinct C3b and C4 human C3b/C4b receptor (CRI, CD35) by
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POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYS:
MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE !
LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A
CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
                                                                                                                                                                    European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                              SPECIFICITY.
MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F
SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
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87168191.
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annotation
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7 X SUSHI (SCR) REPEATS, LONG HOMOLOGOUS
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structural and functional relationships among human,
mouse, and rat proteins.";
J. Immunol. 158:1315-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z50051; CAA90391.1; HSSP; P10998; 1VVC.
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15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00084; sushi; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRACMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S SUBUNIT: DISSUFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS. SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
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                                                                                                                                                                                                                                                                                                                                                                     pathway;
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                              Plasma;
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                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Repeat; Sushi; Signal BY SIMILARITY.
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8 X SUSHI (S
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                                                                                                                                                                                                                                                                                                                  PROTEIN ALPHA CHAIN
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Rattus.
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bovine, rabbit,
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                                                                                                                                                                  C4BP_MOUSE D18607;
P08607;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
--- PTNDTING PROTEIN PRECURSOR (C4BP).
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of the serum complement system.";
Biochemistry 26:4668-4674(1987),
-!- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
(C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B.
ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3
                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Medanfia: Sciurognathi; Muridae; Murinae; Mus.
                                                                                      Kristensen
                                                                                              SEQUENCE FROM N.A. MEDLINE; 88024997.
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                                                                      Kristensen T., Ogata R.T., Chung L.P.,
"cDNA structure of murine C4b-binding ]
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Similarity 29.9%;
94; Conservat'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                             PPPAIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMVYCKPSGEW-EIS-VS-CA 116
GNGNWSSLPTCEF-DCDLPPAIVNGYYTSM-VYSKIT-LVTYECDKGYRLVGKAIIS-CS
                                       GF--WSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCT
                                                                              TVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVIECQ
                                                                                                                                                                                                                                                                                      PPRRNTEILTGSWSDQT-YPEGTQAIYKCRPGY-RSLGNVIMVCR-KGEWVALNPLRKCQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:88229; C4BP.
                                                                                                                       IPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD
                                                                                                                                                                FPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLVGSPFIGCTVVNK 228
                                                                                                                                                                                                          KRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTND 119
                                                                                                                                                                                                                                                 KKHCRNPGYLDNG-Y-VNGETI-TFGSQIEFSCQEGFILVGSST-SSCEVRGKGVAWSNP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M17122; AAA37312.1; ALT_INIT. A27117; NBMSC4.
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27.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4B-BINDING PROTEIN.
6 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 6.
                                                                                                                                                                                                                                                                                                                                                                        Score 402; DB 1; Let Pred. No. 7.44e-78; 74; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Repeat; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
41E137CB8D8C6321 CRC64;
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 COMPLEMENT ACTIVATION TO PROVIDE HEAD IN THE TEQUIATORS OF COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

-!- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

-!- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                       Isaacs S.N., Kotwal G.J., Moss B.;
"Vacchia virus complement-control protein prevents
antibody-dependent complement-enhanced neutralization and contributes to virulence.";
                                                                                                                                                                                                                                                                                                                                                                       Paoletti E.;
"The complete DNA sequence of Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                     Goebel S.J., Johnson G.P., Perkus
                                                                                                                                                                                                                                                                                                                                     STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-COPENHAGEN;
MEDLINE; 91021027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kotwal G.J., Moss B.; "Analysis of a large cluster of nonessential genes deleted vacchnia virus terminal transposition mutant."; Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kotwal G.J., Moss B.; "Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
COMPLEMENT CONTROL PROTEIN PRECURSOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCP_VACCV
P10998;
                                                                                                                               Barlow P.N
                                                                                                                                       Wiles A.P., Shaw G., Bright J.,
                                                                                                                                                                  STRUCTURE
                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                              Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                 COMPLETE GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88318974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccinia virus (strain WR),
                                                                                                             "NMR studies of a viral protein that mimics the regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROTEIN C3) (28 KD PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235
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                                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                                           S.J., Johnson G.P., Perkus M.E., Davis S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335:176-178(1988).
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                                                                                                                                                      97446168
                                                                                                                                                                 BY NMR OF 146-263
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                                                                                                                                                                                                                                                                                                                                                                                    vaccinia
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                                                                                                                                      Perczel A., Campbell I.D.,
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(VCP) (SECRETORY PROTEIN
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                                                                                                                                                                                                                                                                                                                     S.W.,
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                                                                                                                                                                                                                                                                                                                    Winslow J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                             Winslow
                                                                                                                                                                                                                  of infectivity
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DISULFID
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                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
SEQUENCE FROM N.A.
MEDLINE; 89168432.
Johnston G.I., Cook R.G., McEver R.P.;
Johnston G.I., Cook R.G., mcEver R.P.;
"Cloning of GMP-140, a granule membrane protein of platelets and endothelium: sequence similarity to proteins involved in cell
                                                                                                                                                                                                                                                                                                                                                                                              LEM3_HUMAN P16109;
                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
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1VVD; 03-DEC-97.
1VVE; 03-DEC-97.
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A31005; WMVZSP.
                                                                                                                                                                                                                                           OR GMRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WINDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
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80; Conser
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34.2%;
                                                                                                                                                                   Catarrhini;
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                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Mammalia;
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4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
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BY SIMILARITY.
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37; 1
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Pred. No. 5.28e-74;
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                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           830 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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adhesion and inflammation."; Cell 56:1033-1044(1989).
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"The P-selectin gene is highly polymorphic: reduced frequency of the
pro715 allele carriers in patients with myocardial infarction.";
Hum. Mol. Genet. 7:1277-1284(1998).
-i. FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
-i. FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
-i. FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
-i. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
-i. SUBCELLULAR LOCATION RECEPTOR PROTEIN
-I. SUBCELLULAR LOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bajorath J., Stenkamp R., Aruffo A.; "Knowledge-based model building of proteins: concepts and examples."; protein Sci. 2:1798-1810(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 160-199 MEDLINE; 97057176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 35:13733-13744(1996).
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                     PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herrmann S.M., Ricard S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-STRUCTURE MODELING OF 42-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure and function of the epidermal growth factor domain of P-
                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                              EMBL;
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FRAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.
DATABASE: NAME=PROW; NOTE=CD guide CD62P entry;
WMW="http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE CELL SURFACE.
                                                                                                                                                                      A30359;
                                                                                                           173610
                                                                                                                                                1FSB; 01-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         M60234; AAA35910.1;
M60217; AAA35910.1;
M60218; AAA35910.1;
                                                                                                                             1KJD; 03-APR-96.
                                                                                                                                                                                                            M60233; AAA35910
                                                                                   PR00343; SELECTIN
                                       PS00022;
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                        PS00615;
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                                                                                                                                                                      A30359
                                                                                                                                                                                                                                                 AAA35910.1;
AAA35910.1;
AAA35910.1;
AAA35910.1;
AAA35910.1;
AAA35910.1;
AAA35910.1;
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; AAA35910.1;
; AAA35910.1;
; EGF_1; 1.
; EGF_2; 1.
; C_TYPE_LECTIN_1;
; C_TYPE_LECTIN_2;
                                                                                                                                                                                        NOT_ANNOTATED
                                                                                                                                                                                                                               JOINED.
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PFAM; PF000059; lectin_c; 1.
PFAM; PF00084; sushi; 9.
Cell adhesion; Transmembrane;
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   Local Similarity les 85; Conser
                                830 AA;
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   Conservative
                                                                                                                     Sushi;
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         14.8%;
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         Score 376; DB 1;
Pred. No. 1.02e-70;
                                                   /FTId=VAR_004194.
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                                     WITH MYOCARDIAL INFARCTION)
/FTId=VAR_004195.
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C-TYPE LECTIN (SHORT FO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; EGF-like domain;
at; Polymorphism; 3D-structure.
                             FBC407BA2579F6EB CRC64;
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                                                   (REDUCED FREQUENCY IN PATIENTS
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              Length 830;
                                                                                                      (PROBABLE).
Indels 23;
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Gaps
21;
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EMBL; D10056; BAA00945.1; -. EMBL; S70439; AAB30789.1; -. EMBL; Y11356; CAA72190.1; -.
                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             "Structure of the human beta-2-glycoprotein I gene.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
'- FUNCTION: BINDS TO VARIOUS KINDS OF NEGARIVELY CHARGED SUBSTANCES
SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q01339;
Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1993 (Rel. 38, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
APOH OR B2GPI.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein I (apolipoprotein H).";
Riochem. Biophys. Res. Commun. 200:1521-1528(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nonaka M. Matsuda Y. Shiro
"Molecular cloning of mouse
"are to chromosome 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sellar G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                Kristensen T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization, expression and evolution of mouse beta rivcoprotein I (apolipoprotein H).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     whitehead A.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 AFAYGSSCKFECQPGYRVRGLDMLRCIDSGHWSA--PLPTCEAISC-EPLESPVHGSMDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                            TISSUE SPECIFICITY: PLASMA.
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BA/J; TISSUE-LIVER;
94242017.
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mouse beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T., Moriwak K., Natsuume-Sakai S.;
2-glycoprotein I and mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345
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SIGNAL 1
CHAIN 20
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                                                                                                                                               LEM3_RAT STANDARD; PRT; 768 AA.

P98106;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GCD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                               MEDLINE; 94333817.
                                                                                         Eutheria; Rodentia;
                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                    199
               Auchampach J.A.,
                                                              SEQUENCE FROM N.A.
Auchampach J.A., Oliver M.G., Ando
"Cloning, sequence comparison and
                                                                                                                                                                                                                                                                                                          255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                                                                                          PNGD-YSPLRIK 265
                                                                                                                                                                                                                                                                                                                                      KATVLYQGMRVK 281
                                                                                                                                                                                                                                                                                                                                                                                      NGYVNYPAKPVLLYKDKATEG--CHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFPPRPE 212
                                                                                                                                                                                                                                                                                                                                                                  NG--S-PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI 254
                                                                                                                                                                                                                                                                                                                                                                                                                               VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I:88058; APOH.
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29.4%;
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                                                                                           Sciurognathi; Muridae;
                                                                                                           Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
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Pred.
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BY SIMILARITY
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G -> R (IN
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      and in vivo expression of th
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C83F8A6EBD51C940 CRC64;
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No. 2.38e-69;
   in vivo expression
                                                                                                           Vertebrata;
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                                                                                              Mammalia;
Rattus.
                                                                                                                                                      (GMP-140) (PADGEM)
LE 3) (LECAM3).
    the gene
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       RT encoding rat P-selectin.";

11. Gene 145:251-255(1994).

12. Gene 145:251-255(1994).

12. CI FUNCTION: CA(2+) - DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS

12. CI CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE

13. INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH

14. CI CI CINCETLOUAR LOCATION: TYPE I MEMBRANE PROTEIN.

15. CI SUBCELLOUAR LOCATION: TYPE I MEMBRANE PROTEIN.

16. CI SUBCELLOUAR LOCATION: TYPE I MEMBRANE PROTEIN.

17. CI CI SUBCELSTOITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,

17. CI CI INDUCTION: ACCTE INFLAMATION (PROBABLY).

18. CI INDUCTION: ACCTE INFLAMATION (PROBABLY).

19. CI CI SIMILARITY: CONTAINS 1 COTYPE LECTIN FAMILY DOMAIN.

19. CI SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

19. CI SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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HSSP; P16109; IFSB.
PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01615; C_TYPE_LECTIN_1; 1
PROSITE; PS00615; C_TYPE_LECTIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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(POTENTIAL)

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                                                                                                                                                                                                "Molecular cloning of the b subunit of mouse coagulation factor XIII and assignment of themsene to chromosome 1: close evolutionary relationship to complement factor H.";

Genomics 15:335-42(1993).

-i- FUNCTION: THE B CHAIN OF FACTOR XIII IS NOT CATALLYTICALLY ACTIVE, BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND REGULATE THE RATE OF TRANSGLUTAMINASE FORMATION BY THROWBIN.

-i- SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.
-i- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER AND KIDNEY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F13B_MOUSE STANDARD; PRT; 668 AA. Q07968; Q07968; Q1-FEB-1995 (Rel. 31, Created) Q1-FEB-1995 (Rel. 31, Last sequence update) Q1-FEB-1995 (Rel. 31, Last sequence update) Q1-FEB-2000 (Rel. 39, Last annotation update) QCAGULATION FACTOR XIII B CHAIN PRECURSOR (EC 2.3.2.13) (PROTEINGLUTAMINE GAMMA-GLUTAMYLTRANSFERASE B CHAIN) (TRANSGLUTAMINASE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-B10.D2/OSN; TISSUE-LIVER; MEDLINE; 93224141.
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CARBOHYD
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license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).
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Pred. No. 2.94e-68;
53; Mismatches 13(
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ENDOCYTOSIS SIGNAL (PROBABLE).
26FD7E8A5F3F1316 CRC64;
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PIR; A46013; A46013.
HSSP; P10998; IVVC.
MGD; MGI:88379; F13B.
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                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
                YHENMRRPY 326
                                                            NNIQLKWKY 472
                                                                                                                                                                                      PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSC-EE-KSCDNP-YIPNGD
                                                                                                                                                                                                                                                                                  DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVE----ISC-KSPDVINGS
                                                                                                                                                                                                                                                                                                                          YR--H-GERVHIECELNFVIQGSEELLC-ENGKWT-EPPKCIEEKEKVACEQPPSVENGV
                                                                                                Y-SPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL
                                                                                                                                         VYDGLLASYTTGSSVEYRC-NEYYLLKGSETSRCEQGAWSSPPVC-LEPCTI-DVDHMNR
                                                                                                                                                                                                                                    AHPHSEIYYSGDKVTYRCGGGYSLRGSSTITCNRGRWTLPPECVENIENCKPPPDIANGV
                                                                                                                                                                                                                                                                                                                                                                           GVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEV--VKCLPVTAPENGKIVSSAMEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKCRPGY-RSLGNVI-MV-CRKGEWVALNPLRKCOKRPCGHPGDTPFGTFTLTGGNVFEY
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90; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sushi; 8
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29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
57; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 363; DB 1;
Pred. No. 3.61e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coagulation; Repeat; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 X SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COAGULATION FACTOR XIII B CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 28;
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01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4BPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C4B-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4BP_BOVIN
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Immunol. 153:4190-4199(1994).

TEUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DEGROLATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillarp A., Thern A., Danidaech b., Bovine C4b binding protein. Molecular cloning of the alphanaproteine C4b binding protein. Molecular cloning of the alphanaproteine complements are provided structural background for lack of complements.
                        DISULFID DISULFID
                                                                                                               DISULFID DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 (Rel. 35
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7 (Rel. 35
9 PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA CHAIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                       C4B-BINDING PROTEIN ALPHA CHAIN.
8 x SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 7.
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Best Local
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Q1-ARR-1993 (Rel. 25, Created)
Q1-ARR-1993 (Rel. 25, Last sequence update)
Q1-ARR-1993 (Rel. 25, Last sequence update)
Q1-ARR-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
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DISULFID
CARBOHYD
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                                                                                                                                       Blood 80:795-800(1992)
-!- FUNCTION: CA(2+)-DF
                                                                                                                                                                                                                                                              Weller A., Isenmann S., Vestweber D.;
"Cloning of the mouse endothelial selectins. E
and P-selectin is inducible by tumor necrosis
J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEM3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135
                                                                                                                                                                        selectin.
                                                                                                                                                                                   Sanders W.E. Jr., Wilson R.W.,
"Molecular cloning and analysi
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 92345617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 VIVKT-D-YSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVVWSDPLPQCIIAKCEPPPTI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 NETRFETGTTLRYTCRPGYRISSRKNFLICDGTDNW-KYKEF--CVKKRCENPGELLNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                         FUNCTION: CA(2+) DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WELLBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
   INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPRCTLKPCDYPDIKH 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYIECKEVCCPEPNLNN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC-DNPYIPNG--D-YS-PLRIKHRTGD-E-I-TYQCRNGFYPATRGNTA-KCTST-GWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCLGLPHIPHALWERYDHQTQTEQQVYDIGFVLSYKCHFGYKPETDGPTTVTCQSNLEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRPLP-SCEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICVQPVVKDGKITSGFGPIYTYQQSIVYACNKGFRLEGDSLIHCEADNSWNPPPPTCELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-DD---GFWSKEKPKCVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNGR-HNGG-DEDF-YTYGSSVTYSCDRDFSMLGKASISCRVENKTIGVWSPSPPSCKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRECDTDG--WTNDIPICEVVKCLPVTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDQTYPEGTQAIYKCRPGYR-SLGNVIMVCR-KGEWVALNPLRKCQKRPCGHPGDTPFGT
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Similarity 26.8%;
85; Conservati
                                                                                                                                                                                                                                                                                                                             92340571
                                                                                                                                                                                                                                                                                                                                                                          Rodentia;
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                   SURFACE
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                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                      analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 357; DB 1;
Pred. No. 1.54e-65;
71; Mismatches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN
INTERCHAIN
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                       Ballantyne C.M.,
                                                                                                                                                                                      of in vivo expression
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BETA CHAIN) (POTENTIAL).
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PROSITE; PS5004
PFAM; PF00008; 1
PFAM; PF00059;
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DOMAIN
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PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1;

PROSITE; PS00611; C_TYPE_LECTIN_2;

PROSITE; PS00611; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; M72332; AAA37712.1; -.
PIR; A42755; A42755.
                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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SIMILARITY:
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
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                                                                                                                                                                                                                                                                                                                                                                        Signal; Sushi; Repeat
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sushi; 8.
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EGF-LIKE
8 X SUSHI
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 6.
SUSHI 7.
SUSHI 7.
                       POTENTIAL.
                                                         ENDOCYTOSIS SIGNAL (PROBABLE).
A -> E (IN REF. 2).
                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN (SHORT FO
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                EMBL;
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG PRECURSOR (CCPH).
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92260674.
Albrecht J.-C., Fleckenstein B.;
"New member of the multigene family of herpesvirus saimiri.";
J. Virol. 66:3937-3940(1992).
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Newman C., Wittmann S., Craxton M.A.,
Honess R.W.;
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Viruses; dsDNA viruses, no I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of the herpesvirus saimiri genome.";
Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
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3L; X64346; CAA45626.1; -.
3L; X64346; CAA45627.1; -.
3L; X60283; CAA42823.1; -.
3L; X60283; CAA42822.1; -.
3; B42534; WMBE2E
3; A42534; WMBE1E.
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nes 77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).
SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
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larity 26.9%;
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Pred. No. 9.54e-62,
52; Mismatches 13
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HSSP; P10998; 1VVC.
PFAM; PF00084; sushi; 4
Signal; Repeat; Sushi;
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SIGNAL
CHAIN 2
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P05160;
13-AUG-1987
01-AUG-1990
15-JUL-1999
COAGULATION
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SEQUENCE OF 2-661 MEDLINE; 87026535.
                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                              CHAIN).
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                                                     Biochemistry
                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                  "Nucleotide
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Loninose A., McMullen B.A., Fujikawa K.,
"Amino acid sequence of the b subunit of
composed of ten repetitive segments.";
Biochemistry 25:4633-4638(1986).
[3]
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"Two genetic defects in a patient with complete deficiency of the b-
subunit for coagulation factor XIII.";
Blood 82:145-150(1993).

-i- FUNCTION: THE B CHAIN OF FACTOR XIII IS NOT CATALYTICALLY ACTIVE,
BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND REGULATE THE RATE
OF TRANSGLUTAMINASE FORMATION BY THROMBIN.

-i- SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.

-i- SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.

-i- SUBUNIT: DEFECTIVE WOUND HEALING, AND HABITUAL ABORTION.

-I- SIMILARITY: CONTAINS 10 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grundmann U., Nerlich C., Rein T., Zettlmeissl "Complete cDNA sequence encoding the B subunit Nucleic Acids Res. 18:2817-2817(1990).
EMBL; M64554; AAA51821.1; ALT_SEQ.

EMBL; M14057; AAA88042.1; -.

EMBL; X5183; CAA3613.1; -.

PIR; A23839; A23830.

PIR; A36397; A36397.

PIR; A36397; A36397.

PIR; S09980; S09980.
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                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Run on: MPsrch_pp Sequence: Description: Perfect Score: Tabular output not generated. Statistics: Database: Post-processing: Scoring table: Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Gap] Minimum Match Listing first Thu Jun 8 21:46:38 2000; MasPar time 30.28 Seconds 753.376 Million cell updates/sec 22,8878 seqs, PAM 150 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 329 sptrembl12 Mean 43.988; Variance 63.846; scale 0.689 1:sp_archéa 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_4nvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus ð9334122 residues 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Score	Query Match 1	Length DB	Ü	IB	Description	Pred. No.
_ ;	2539	100.0	449	4	Q14570	COMPLEMENT FACTOR H PR	0.00e+00
N	1236	48.7	669	9	Q28085	CCP MODULES 3-12, WITH	0.00e+00
ω	603	23.7		3	Q91275	COMPLEMENT REGULATORY	1.99e-130
4	476	18.7		4	Q14006	COMPLEMENT H FACTOR (F	1.99e-95
ъ	438	17.3		11	Q61407	COMPLEMENT FACTOR H-RE	4.10e-85
S	436	17.2		14	Q9WRU2	COMPLEMENT BINDING PRO	1.42e-84
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8	429	16.9		14	040912	ORF 04.	1.10e-82
و	428	16.9		14	P88903	ORF 4.	2.05e-82
10	426	16.8	522	σ	Q28769	COMPLEMENT RECEPTOR (F	7.11e-82
11	423	16.7	2014	σ	Q29530	COMPLEMENT RECEPTOR 1	4.5/e-81
12	412	16.2	1911	σ	Q29528		4.14e-78
13	409	16.1	2039	4	Q16745		2.64e-77
14	409	16.1	2489	4	Q16744		2.64e-//
15	403	15.9	661	6	Q29531	COMPLEMENT RECEPTOR 1	1.07e-75
16	398	15.7		14	P87616	41KBP FRAGMENT FROM LE	2.33e-74
17	389	15.3	522	σ	Q28797	UNKNOWN PROTEIN (FRAGM	5.90e-72
18	388	15.3	560	σ	Q22328	COSMID T07H6.	1.09e-71
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Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                               Thesis (1993), Inmunologia, Hospital Trias I Pujol, Spain.
EMBL; X07523; CAA30403.1; -.
EMBL; M12383; AAA52013.1; -.
EMBL; U56979; AAB01987.1; -.
EMBL; Z29665; CAA82763.1; -.
EMBL; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 88134059.
RIPOCHE J., DAY A.J., HARRIS T.J.R., SIM R.B.;
"The complete amino acid sequence of human complement factor H.";
Biochem. J. 249:593-602(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HF OR CFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRISTENSEN T., WETSEL R.A., TACK B.F.; "Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-91/coprotein I, and the Ba fragment of B2."; J. Immunol. 136:3407-3411(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-9 FROM N.A. DOMINGUEZ O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-19 FROM N.A. VIK D.P., WILLIAMS S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 226-449 FROM N.A. MEDLINE; 86169701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00084; sushi; 7.
                                                                                                                     449 AA;
                                                                                                                                                                             18
449
      100.0%; Score 2539; DB 4;
                                                                                                               51033 MW; 61231E1B CRC32;
                                                                                                                                                                                   POTENTIAL.
            Length 449;
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247 SY--RGYFP 253

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q28085 PRELIMINARY; PRT; 669 AA.
Q28085; O1-NOV-1996 (TremBLrel. 01, Created)
O1-NOV-1996 (TremBLrel. 01, Last sequence update)
O1-NOV-1999 (TremBLrel. 12, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                     PFAM;
                                                                                                                                                                                                                                                                                                                                                                                   SOAMES C.J., DAY A.J., SIM R.B.;
"Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).
                                                                                                                                                                                                                                                                                                                                                            EMBL; X98697; CAA67257.1; -. HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae;
260 SPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGLYH
                       187 RPELSKYRGOOKITYECKKGFFPEIRGTDATCTRDGWVPVPRCAWKPCSYPVIKHGRLYY 246
                                                                                                                 140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                         67
                                                                                                                                                                                       08
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                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                        7 LAEGNOFEYGAKVYYTCDEGYQMYGEMNFRECDINGWINDIPICEYYKCLPYTEPENGKI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSIGNYIMVCRKGEWVALNPLR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                       GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDY
                                                                                     GQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIPNGVY
                                                                                                                                    FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                             LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCTLKPCDYPDIKHGGLYHENMRRPYFPV 347
                                                                                                                                                                                                                                                                                                                                                 PF00084; sushi; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR
                                                                                                                                                                                                                                                 48.7%;
Similarity 61.4%;
153; Conso
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                                                                                                                                                                                                                                                                                                        669 AA;
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                  669
75683 MW; FAF0D174 CRC32;
                                                                                                                                                                                                                                                         Score 1236; DB 6;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                           35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.00e+00; 0; Mismatches 0;
                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                       Length 669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q14006 PRELIMINARY; PRT; 657 AA.
Q14006;
Q1-NOV-1996 (TremBLrel. 01, Created)
O1-NOV-1996 (TremBLrel. 12, Last sequence update)
O1-NOV-1999 (TremBLrel. 12, Last annotation update)
MEDLINE; 88025472.

DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B., "Sequence analysis of a cDNA clone encoding thuman complement factor H.";
                                                                                                                                                                                                                                                                                                                                           HF.
Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91275 PRELIMINARY; PRT; 1053 AA.
Q91275;
Q91275;
Q01275;
Q01275;
Q01-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 12, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
Paralabrax nebulifer (barred sand bass).
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENT H FACTOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAHMEN A., KAIDOH T., ZIPFEL P.F., GIGLI I.; aputative "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAHMEN A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 EASYPGGROVRVGCNVGY-S-GFFKLVCVEGKWETRGA--KCOPRSCGHPGDAOFADFHL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDYSPL-RIKHRTGDEITYQC-RNGFYPATRGNT--AKCTSTG-WIPAPRCTLKPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPISQKIIYKENERFQYKCNMGYEYSERGDA-V--CTESGWRPLPSCEEKSCDNPYIPN
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                                                                                                                                                                                                                                                                                                                     Chordata; Craniata;
Catarrhini; Hominida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117597 MW; ODF68EDB CRC32;
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                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Mammalia;
                                                       the C-terminal
                                                                                                   HARRIS T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1053;
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                                      SIM R.B.;
al end of
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                                                                                                                                                 Query Match
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EMBL; M17517; AAA52016.1; -.
HSSP; P08603; 1HFH.
PFAM; PF00084; sushi: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q61407
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                             EMBL; M29010; AAA37415.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                       VIK D.P., MUNOZ-CANOVES P., KOZONO H., CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 CSQ-PPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMCKW-S-SP-PQ 351
                                                                                                                                                                               PFAM; PF00084; sushi; 7
SEQUENCE 452 AA; 516
                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                  CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                   VIK D.P.,
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
296 WIPAPRCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                          236 SGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRIGDEITYQCRNGFYPATRGNTAKCTSTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 18.7%;
Local Similarity 27.5%;
es 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CNELPPRRNTEILTGSWSDQ-TYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK 61
                          75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPV 108
                                                                                      15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                              17.3%;
Local Similarity 56.4%;
es 53; Conservation
                                                                                                                                                                                                                                                                                                                   Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKCFEGFGIDGPAIAK-CLGEKWSHP-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWSEPPKC-LHPC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEPPOCKDSTGKCGPPPPIDNGDITSFPLSYYAPASSYEYQCQN-LYQLEGNKRITCRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEKPKCVEISC-KSPDVINGSPIS-QKIIYKENERFQYKCNMGYE-YSERGDAVCTESGW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGERVRYQCRSPYEMFGD-EEVMCLNGNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQVTYTCATYYKMDGASNVTCINSR-WT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWIPAPRCTLKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPLPSCEEKS - - CDNPY - IPNGDYSPLRIK - HRTGDEITYQCRNGFYPATRGNTAKCTST
                                                                                                                                                                                                                                            (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 MUNOZ-CANOVES P., KOZONO H., MARTIN L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307
                                                                                                                                                                                  51602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 476; DB 4; Length 657; Pred. No. 1.99e-95; 72; Mismatches 132; Indels 23;
                                                                                                                         16;
                                                                                                                                   Score 438; DB 11;
Pred. No. 4.10e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F4AB5238 CRC32;
                                                                                                                                                                                  45C0BF61 CRC32;
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 AA
                                                                                                                                                                                                                                                                            MARTIN L.G.,
                                                                                                                                                    Length 452;
                                                                                                                           Indels
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Best Local
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Best Local S
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Q9WRU2;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT BINDING PROTEIN.

17577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta rhadinovirus 17577.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q61405
Q61405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TremBLrel. 01, Created)
01-NOV-1996 (TremBLrel. 01, Last sequence update)
01-NOV-1999 (TremBLrel. 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                        "Identification and sequence analysis of four complement factor related transcripts in mouse liver.";
J. Biol. Chem. 265:3193-3201(1990).
EMBL; M29007; AAA37413.1;
HSSP; P10908; 1VC.
PFAM; PF00084; sushi; 4.
SEQUENCE 303 AA; 34498 MW; 39350FD1 CRC32;
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J. Virol. 73:304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 EKYSVGASVELICRPGFTKMQSTVSVECLSNGTWTAPNA--KCHRKKCPTPQELLNGEYI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIK D.P., MUNOZ-CANOVES P., KOZONO H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 90153969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAPLIN D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 PENGKIVSSAMEDDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 ITNGKY--HPVK-DF-YQYLDTVTFSCNRDFSLVGDEMTTCISNT-WNKPFPRCEQITCS 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 VTSGEDAFKYGTNITYKCNEGYQLLGSMYRICMLKDDLKTVDWEPKAPICDIEKCKPPPQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 SPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 APNIAHGKLLTGSSSVYKYGQSVTIGCETGFTLIGSEISTCKDSSWDPPLPTC 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 17.2%;
Local similarity 30.9%;
236 SGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 LTGG-NVFEYGVKAVYTCNEGYQLLGE-IN-Y--REC-DTDGWINDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 QTYPEGTQAIYKCRPGYRSLGNVIMV-C-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
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AF083501; AAD21332.1; -
                                                                                     TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG
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                                                                                                                                                                      17.1%;
Similarity 55.3%;
52; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645 AA; 71526 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Mammalia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.42e-84;
50; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 436; DB 14;
Pred. No. 1.42e-84;
                                                                                                                                                                                    Score 433; DB 11;
Pred. No. 9.20e-84;
17; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60FB82D6 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARTIN L.G.,
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                                                                                                                                                                                                                                                                         Length 303;
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040912 PRELIMINARY;
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T 01-JAN-1998 (TrEMBLrel. 12, Last annot
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                        Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
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SEQUENCE FROM N.A
                                                                                                                                                                                                                          P88903;
01-MAY-1997 (TIEMBLIEL 03, Created)
01-MAY-1997 (TIEMBLIEL 03, Last seq.
01-NOV-1999 (TIEMBLIEL 12, Last ann
                                                 RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA D., PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8).";
                                                                                                                                                               Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                      Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                MEDLINE; 97121480
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    P88903
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"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
J. Virol. 71:4187.4192(1997).
EMBL; U93872; AAB62602.1; -.
HSSP; P10098; IVVC.
PFAM; PF00084; sushi; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RCRSGYTTYARNITATCLQGGTW-S-EPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG 89
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Last annotation update)
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Pred. No. 1.10e-82;
59; Mismatches 110; Indels 2
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Last annotation update)
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BIRMINGHAM D.J., LOGAR C.M., SHEN X.P., CHEN W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L77977; AAA99004.1; -.
HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-NOV-1996 (Trembirel 01, Created)
01-NOV-1996 (Trembirel 01, Created)
01-NOV-1996 (Trembirel 01, Last sequence update)
01-NOV-1999 (Trembirel 12, Last annotation update)
COMPLEMENT RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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120 IPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN--SGYK-I-E--GDEEM
                                                              163 TPICEIIPCGLPPTIA-NGDFISTSRE---YFPYGSVVTYRCNLGSGRKKLFELVGEPSI 218
                                                                                                                                                                                            105 TRKSCRNPKD-PVNGMVHVIKDI-QFGSQINYSCNKGYRLIGSSSATCIISGNTVIWDNE 162
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HSSP;
PFAM;
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Science 274:1739-1744(1996).
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MOORE P.S., BASHOFF C., WEISS R.A., CHANG Y.;

"Molecular mimicry of human cytokine and cytokine response pathway
                                                                                                                                                                                                                                                                                                                          52 EQLPFARPIN-LIDA-SE--FPVGTYLKYECLPGYHGKPFSI-ICLKNSVWTSAKD--KC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 PLRIKHRTGDEITYQCRNGFY-PATRGNTAKCTST 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 PTP-NEKPNGNV-FQ-RSNYTEPPTKPEDTHTAAT 315
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                                                                                                                                                                                                                                                                  4 NELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKC 62
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                                                                                                                                                                                                                                                                                                                                                                                                h 16.8%; Score 426; DB 6; Length 522; Similarity 32.1%; Pred. No. 7.11e-82; 111; Conservative 74; Mismatches 119; Indels 42;
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Similarity 29.8%; Pred. No. 2.05e-82;
82; Conservative 59; Mismatches 110
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Q29530 PRELIMINARY; PRT; 2014 AA.
Q29530;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
Q29528
Q29528;
Q1-NOV-1996
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1391 FPVGTSLNYECRPGY--FGKMFSISCLENLVWSSVED--NCRRKSCGPPPE-PFNGMVHI 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Immunol. 153:691-700(1994).
EMBL; L24920; AAA51438.1; -.
HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 9429799.

BIRMINGHAM D.J., SHEN X.P., HOURCADE D., NICKELLS M.W., ATKINSON J.

"Prinary sequence of an alternatively spliced form of CR1. Candidat

for the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Primates; Catarrhini; Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00084; sushi; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erythrocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                 1679 PRCTVKSCDDFLGQLPHGRVLFPLNLQ 1705
                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                         245 EEKSCDNP-YIPNGDYSPLRIKH-RTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIP-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 16.7%;
Local Similarity 29.1%;
hes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCTSKDDQVGIWSGPAPQCIIPNKCMPPNVENGVLVSVNRSLFSLNEVVEFRCQPGFVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRGNTA-KCTSTG-WIP-APRCTLKPCD-Y-PDIKHG-GLYHENMR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRGAASLHCTPQGDWNPEAPICTVKSCDDFLGQLPHGRVLFPLNLQ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPRHVQCQALNKWEPELPSCS-RVCQPPPEILHGEHTPSHQDFSPGQEVFYSCEPG-Y-D 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERGDAYCTE-SGWRP-LPSCEEKSCDNP-YIPNGDYSPLRIKHRTGDEITYQCRNGFYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STNKCTAPEVENAIRVPGNRSFFSLTEIVRFRCQPGFVMVGSHTVQCQTNGRWGPKLPHC 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTDT-QFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGD 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYSNNRAS---FHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCI 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGNVFEYGVKAVYTCNEGYQLLGE--INYRECDTD-GWTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT 81
                                                                                                                                                                                                                      PRCTLKPCD-Y-PDIKHG-GLYHENMR 323
                                                                                                                                                                                                                                                                                                                                                                                 S-RVCQPPPEILHGEHTPSHQDNFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWSPEA 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2014 20
2014 AA;
   (TrEMBLrel. 01, (TrEMBLrel. 01,
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 423; DB 6; Length 2014;
Pred. No. 4.57e-81;
74; Mismatches 119; Indels 3
   Created)
Last sequence update)
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                                                                                                         1911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 39;
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Best Local Similarity 29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1303 FPVGTSLNYECHPGY--FGRMFSISCLENLVWSSVED--NCRRKSCGTPPE-PFNGMVHI 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1995) to the EMBL/GenBank/DDBJ EMBL; L39791; AAA62170.1; -. HSSP; P08603; 1HCC. PFAM; PF00084; Sushi; 29. NON_TER 1911 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Last annotation update) COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q16745
Q16745;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEMENZA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1534 S-RVCQPPPEILHGEHTPSHQDKFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWSPEA 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1417 FYSNNR-TS--FHSGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGAMSSPPPRCI 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1591 PICTVKSCD 1599
EMBL; L17418; AAB60694.1; JOINED.
EMBL; L17390; AAB60694.1; JOINED.
EMBL; L17391; AAB60694.1; JOINED.
EMBL; L17392; AAB60694.1; JOINED.
EMBL; L17393; AAB60694.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94065175. VIK D.P., WONG W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Ci
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENT RECEPTOR 1.
                                                                                                                                                  SEQUENCE FROM N.A. VIK D.P., WONG W.W.; Submitted (JUN-1993)
                                                                                                                                                                                                                                                                  "Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S allele.";
J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 EEKSCDNP-YIPNGDYSPLRI-KHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIP-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 PRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STNKCTAPEVKNGIRVPGNRSFFSLNEIVRFRCQPGFVMVGSHTVQCQTNNRWGPKLPHC 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTDT-QFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKEAPICEIISCKPPPTISNGD 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGNVFEYGVKAVYTCNEGYQLLGE--INYRECDTD-GWTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1911 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210173 MW; 03D640C2 CRC32;
                                                                                                                                                     to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 412; DB 6;
Pred. No. 4.14e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1911;
                                                                                                                                                              databases
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RESULT
AC Q1
DT Q1
DT Q1
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Best Local
                                                                                                                O16744 PRELIMINARY; PRT; 2489 AA. 016744; O1-NOV-1996 (TIEMBLrel. 01, Created) 01-NOV-1996 (TIEMBLrel. 01, Last sequence update) 01-NOV-1999 (TIEMBLrel. 12, Last annotation update) 01-NOV-1999 (TIEMBLRE) 12, Last annotation update)
Homo sapiens (Human).
Eukaryota; Metaga; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
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Submitted
                                               234 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
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J. Immunol. 151:6214-6224(1993).
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                                                                                                                                                                                                                                                                                                                                        63 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMYHYIK 119
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EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                   IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 233
                                                                                                                                                                                                                                                 G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 176
                                                                                                                                                                                                     GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
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L17427; AAB60695
L17428; AAB60695
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L17424; AAB60695
L17425; AAB60695
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272846 MW; 5869B6F9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 409; DB 4; Le
Pred. No. 2.64e-77;
66; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2489;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels 36;
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                                                                                                      188
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Best Local 9
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 15
Q29531
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SEQUENCE
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J. Immunol. 153:691-700(1994).
EMBL; L24921; AAA51439.1; -.
HSSP; P10998; 1VVC.
PFAM; PF00084; sushi; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
CHAIN
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BIRWINGHAM D.J., SHEN X.P., HOURCADE D., NICKELLS M.W., ATKINSON J.P.;

"Primary sequence of an alternatively spliced form of CR1. Candidate
for the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
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                                                                                                             245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA- 299
                                                                                                                                                 189 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                    139 IVSSAMEPDREYHFGQAVREVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                     326 PTCEVKSCD 334
                                                                                                                                                                                                                                                                                             209 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPPRVKCQALNKWEPELPSC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 GNVFEYGVKAVITCNEGYQLLGE--INYREC-DIDGWINDIFICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 FPIGTYLNYECRPGYYGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPD-PVNGMVHVI 93
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Local Similarity 31.1%;
ses 96; Conservative
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   PRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 AA;
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>661
661
72966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 403; DB 6; Length 661; Pred. No. 1.07e-75; 66; Mismatches 111; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
COMPLEMENT RECEPTOR 1.
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Search completed: Thu Jun Job time : 34 secs.

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21:47:12 2000

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:49:10 2000; MasPar time 13.73 Seconds 738.315 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: >US-09-316-163-14 (1-428) from US09316163.pep 371 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428

Scoring table:

PAM 150 Gap 11

Searched: 188963 seqs 23686106 residues

Post-processing: Minimum Match 0%/ Listing/first 45 summaries

Database:

Statistics: Mean 34.511; Variance 134.258; scale 0.257 a-geneseq36 1:geneseqp

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1	Result No.
1385 7212 7212 737 445 446 446 446 446 439 439 439 439 433 436 436 436 436 436 436 436 436 436	Score
41.1 27.9 15.9 13.2 13.2 13.2 13.2 13.2 13.2 13.2 13.1 13.0 13.0 13.0 13.0 13.0 13.0 13.0	Query Match
240 5718 5718 5718 5718 5719 5719 5719 5719 5719 5719 5719 5719	Length 1
	DB
W39154 Y090155 Y090155 Y090155 R289557 R28555 W473147 W473147 W473147 W473147 W473147 R285560 R285560 R285571 R28567 R28567 R28566	ID
Human partial Compleme Clone prabspr410 CFH r Human complement facto Human C4 binding prote CRI-4 (99H, 103E) anal CRI-4 (78T, 79D) analo Amino acid sequence of Human complement recep CRI-4 (85R, 87N) analo CRI-4 (109N, 110A, 111 CRI-4 (109N, 110A, 111 CRI-4 (64K) analogue. CRI-4 (64K) analogue. Partial human compleme Human complement type CRI-4 (369-376 STKPPIC CRI-4 (347T, 349Y) analogue. CRI-4 (347T, 349Y) analogue. CRI-4 (318R, 319N) analogue. CRI-4 (121Q) analogue. CRI-4 (121Q) analogue. CRI-4 (318R, 319N) ana	Description
1. 44e-13 1. 36e-61 1. 36e-61 1. 36e-61 2. 21e-33 2. 21e-33 2. 21e-33 2. 21e-33 3. 1. 74e-33 1. 74e-33 9. 31e-33 9. 31e-33	Pred. No.

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121 INGSPISOKIIYKENERFOYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNG 180

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363	3	379	389	390	411	416	422	422	423	424	425	426	427	428	430	430	431	431	432	432	433	
10.8	10.8	11.2	11.5	11.6			12.5			12.6	12.6	12.6	12.7	12.7	12.8	12.8	12.8	12.8	12.8	12.8		
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of.	Sequence of soluble co	Deduced sequence of co	Membrane co-factor pro	P-selectin.	Amino acid sequence of	CR1-4 (44T, 47D, 49L)	(35E, 37Y)	(114-1	(921	(94H)	_	(116K, 1	(577, 5	(35E)	CR1-4 (116K) analogue.	_	_		_	CR1-4 (64K, 65T) analo	-4 (266-2	
6.46e-25	6.46e-25	1.48e-26	1.38e-27	1.09e-27	7.44e-30	2.25e-30	5.4Le-3L	5.41e-31	4.26e-31	3.350-31	2.54e-31	2.08e-31	1.64e-31	1.296-31	8.01e-32	8.01e-32	6.30e-32	.30e-				

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RESULT
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09-APR-1997; US-812481.
06-MAR-1997; US-815083.
09-APR-1996; US-630048.
06-MAR-1997; US-038614.
06-MAR-1997; US-038614.
(BARD-) BARD DIAGNOSTIC SCI INC.
Enfield DL, Hass GM, Kinders RJ;
WPI; 97-512742/47.
WP-PSDB; V02791.
                                                                                                                                                                         Human complement factor H homolog protein.

Human complement factor H; immunological mechanism; complement reaction; gene therapy; immune stimulation; haematopolesis regulation; chemotactic; tissue growth activity; anti-inflammatory; tumour inhibition;
                                                                                                                                                     secretory signal.
                                                                                                                                                                                                                                                                                                      Y09065;
06-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H related antigen, or nucleic acid encoding it

Example 6B; F1g 6B; 104pp; English.

This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                        02-OCT-1998; J04448
                                                                                          WO9918200-A1.
                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                               Y09065 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor H related antigen, or nucleic acid encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1998 (first entry)
Clone pRRB9FH410 CFH related protein fragment.
Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09738136-A1.
16-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    urogenital cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 VVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPPRVENGDGIYLKPVYKENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AVRFVCNSGYKIEGDEEMHCSDDGFWGKEKPKCYEISCKSPDVINGSPISQKIIYKENER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCNEGYOLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 37.9%;
Local Similarity 73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYP 216:i:iiiiiii:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCDEGYQLLGEIDYRECDADGWINDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHGRL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIPNG
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                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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Pred. No. 1.44e-122;
26; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                  AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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      QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1991 (first entry)
Human C4 binding protein.
C4bp; monomer; complement protein; pJOD.C4bp.3;
                                  region
                                                                                                    region
                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             short consensus repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA encodes a protein having homology to human complement factor H, which plays a role in the immunological mechanism involving the complement reaction. The protein can also be used as an antigen for preparing antibodies against the protein The cDNA can be used as a probe for gene diagnosis and the gene for gene therapy, as well as for large-scale expression of the protein. The protein may also have immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, anti-inflammatory activity tumour inhibition activity, chemotactic/chemokinetic activity receptor/ligand activity, etc. The protein is identified by the presence of a hydrophobic N-terminal secretory signal region, knowledge of the protein function is not required, as in e.g. methods of expression
                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R13490 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins with secretory signal sequences and nucleotide sequences, useful in control of proliferation and differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-1997; JP-272837.
(PROTT-) PROTEGENE INC.
(SAGA ) SAGAMI CHEM RES CENT.
Kato S, Sekine S;
WPI; 99-264019/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 ENGFISESSSIYILNKEIQYKCKPGYATADGNSSGSITCLQNGWSAQPICIKF 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 YENTRRPYFPVATGQSYSYYCDQNEVTPSGSYWDYIHCTQDGWLPTVPCLRTCSKSDIEI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 MWFKLHDTLDYECYDGYESSYGNTTDSIVCGEDGWSHLPTCYNSSESCGPPPPISNGDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 YFGQVVRFECNSGF-KIEGQKE--MHCSENGLWSNEKPQCVEISCLPPRVENGDGIYLKP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 ILNEETQYNCKPGYATADGNSSGSITCLQNG-WSTQ-PICIKF-CDMPVFENSRAKS-NG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claims 1; Page 55-58; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; X34737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 YYCDQNFVTPSGSYWDYIHCTQDGWSPTVP-C-LRTCSKSDVEIENG-FIS---ESSSIY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDT--YYCTENGWSPPPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-YKENERFQYKCKQGF--VYKERGDA-VCTGSGWNPQPSC-EEM-TC-LTPYIPNGIYT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCI-FHY-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHRIKHRID-DEIRYECKNGFYPATRSPVSKCTITGWIPAPRC-SLKPCDFPQFKHGRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFPQKVYLPWSRVEYQCQS-YYELQGSKYVTCSNGDWSEPPRCISMKPCEFPEIQHGHLY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTCDEGYQLL-GEI-DYRECDADGWINDIPICEVVKCL-PVTELENGRIVSGAAEPDQEY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 21.1%;
Similarity 35.1%;
124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 AA;
/label=
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                              /label= SCR7
                                                                                                                            /label= SCR8
                                                                                                                                                                  /label= C4bp
33. .93
                                                                                                                                                                                                                                                         /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                 . 155
                                  .219
                                                                                                                                                                                                                                 581
SCR6
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Pred. No. 1.36e-61;
72; Mismatches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps 25;
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밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New C4 binding protein fusion proteins and DNA encoding them comprise assemblies of C4bp monomers linked to functional moiety, e.g. AZT, useful as delivery vehicles in diagnosis and therapy Example 1; Fig 1; 105pp; English.

C This sequence was deduced from human hepatocyte (Hep G2) cDNA obtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCR, the first cysteine residue bonds with the third and the second cysteine residue bonds with the furth. This secondary structure is responsible for the conformational flexibility of the C4bp monomer. The invention covers fusion proteins in which the monomer sequence, or a specified subfragment of it, e.g. having 5, 4, 3 or 1 SCR(s) is fused to the C-terminal of a protein such as a viral receptor, cell ligand, a bacterial, viral or parasitic immunogen, enzyme, so concerns fusion, etc. See also Q13243-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Pasek MP, Winkler G, wiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-1991;
378
                                                                                                                                                                                                                               116 WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
                                                                                                                                                                                                                                                              147
                                                                                                                                                                                             203 VENETIGVWRPSPPTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSV 262
                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                              33 NC-GPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNT
                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91-252613/34.
                                                                                                                               IHCDADSKWNPSPPACEPNSCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGYKP 322
                                                                                                                                                                                                                                                             WSHPLPQCEIVKCKPPPDIRNGR-HSG--E-ENFYAYGFSVTYSCDPRFSLLGHASISCT
                                                                                                                                                                                                                                                                                                                  FCIY-KR-CRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVG
                                                                                                                                                                                                                                                                                                                                                             DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNP 58
EISFSCHETSRFSAI-CQGDGTWSPRTPSCGDICNFP-PKIAHGHYKQSSSYSFFKEEII 435
                                                                                                AVC-TGSGWNP-QPSCEEMTCLT-PYIPNGIY-T-PHRIKHRI--DDEI-RYECKNGFYP
                                                                                                                                                                                                                                                                                               SRICRKRPCGHPGDTPFGSFRLAVGSEFBFGAKVVYTCDEGYQLLGEIDYR-EC-DAD-G
                                ATRSPVS-KCTIT-GWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCD
                                                               TTDEPTTVICQKNLRWTPYQGCEALCCPEPKLNNGEIT-QH-RKS-RPANHC-VY-FYGD
                                                                                                                                                                -EN---GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD
                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
138; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%;
llarity 30.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-470888.
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/label= <^
?80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65. .92 /note= "intradomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= C4bp_core
/note= "responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-
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.406
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TR;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 537; DB 1; Le
Pred. No. 5.15e-43;
85; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                     The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR1-4 (99H, 103E) analogue. short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R28557;
19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1992; 303826.
03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R28557 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnosis etc.
Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 92-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atkinson JP, Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 N-GFTTPSQSYMDYLRCTVNG-WEPEVP-CLRQCIFHYVEYGESSYWQRR-YIEGQSAKV
77
                                                                                                                                                                                                22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QCHSGYSLPNGQDTYYCTENGWSPP-PKC
                                            RIVSGAAEPDQEYYFGQVVRFECN-
                                                                                                        GSEFEFGAKVVYTCDEGYQLLGEIDYREC--DADG--WTNDIPICEVVKC-LPVTELENG
                                                                                                                                   IKGIQFGSQIKYSCTKGYRLIGHSS-AECIISGDTVIWDNETPICDRIPCGLPPT-ITNG 134
                                                                                                                                                                   YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV
                                                                         DFIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC
                                                                                                                                                                                                                                105;
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                             543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Ser substituted 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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451. .510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "TRUNCATED'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
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                                                                                                                                                                                                                                             13.2%;
32.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543
                                                                                                                                                                                                                             Score 445; DB 1;
Pred. No. 2.21e-33;
72; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                            -SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQC
                                                                                                                                                                                                                               Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glu (SCR-9)"
                                                                                                                                                                                                                                                            Length 543;
                                                                                                                                                                                                                                Indels 40;
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosis etc.

7 Claim 11; Fig 2 and R11810; 23pp; English.

7 Claim 11; Fig 2 and R11810; 23pp; English.

7 The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

7 168:1255-1270. It encodes the first 8 and a half amino terminal

8 CRS of CR1. The invention concerns analogues of "regulator of

9 C complement activation" proteins or truncated, hybrid or recombinant

9 C complement activation proteins or truncated form and a number of

9 C complement activation variants of it are claimed in which certain

9 C specified substitution variants of it are claimed in which certain

9 C specified substitution variants of it are claimed in which certain

9 C specified substitution variants of it are claimed in which certain

9 C specified substitution variants of it are claimed in which certain

9 C specified substitution variants of it are claimed in which certain

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Best Local :
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short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type I receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1992; 303826.
03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON
                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating auto:immune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atkinson JP, Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP-512733-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R28552 standard;
R28552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                                                                      FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
IVSGAABPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                          FIS--TURE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                        GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                              ITDIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                                                                                                                                                                                                                YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%;
ilarity 32.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rdbeT= SCR-9
/note= "TRUNCATED"
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Lys substituted by Thr (SCR-9)"
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511. 543
/label Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Gly substituted by Asp (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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451. .510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 445; DB 1; L
Pred. No. 2.21e-33;
74; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to suppress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ragment of soluble human complement receptor 1 - useful for treating T-cell or B-cell mediated immune responses e.g. inflammatory responses such as rheumatoid arthritis Disclosure; Fig 1; 54pp; English.

This is an amino acid sequence of the human soluble complement receptor 1 (sCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or B-cell-mediated immune responses to prevent immune response-mediated tissue rejection and destruction or clearance or inactivation of an expressed protein especially from cells that have been treated by gene therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an interferon gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the soluble complement receptor 1 (sCR1). Human; soluble complement receptor 1; SCR1; T-cell; B-cell; mediated immune response; inhibition; tissue rejection; gene therapy; dystrophin; inflammatory response; interferon-gamma secretory response; autoimmune response; neurological response; Alzheimer's disease; parkinson's disease; multiple solerosis; systemic lupus erythematosus; parkinson's disease; multiple solerosis; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; epidermis bullosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidermis bullosa or Hashimoto's disease. Sequence 778 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1998; G01012.
05-APR-1997; GB-006950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-568350/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens. W09845430-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annenkov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANNE/) ANNENKOV A. (CHER/) CHERNAJOVSKY Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hashimoto's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W73147 standard; protein; 778 AA.
189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                            239 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                    83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                              68 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 122
                                                                                                                                                                                                                                                                                                                                                                               7 Match 13.2%;
Local Similarity 32.3%;
les 104; Conservative
                                                                                        IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                     FIS--THRE-NEHYGSVVTYRCHPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI
                                                                                                                                                                                                                                  IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 181
                                                                                                                                                                                                                                                                                 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRV-COPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chernajovsky Y;
                                                                                                                                                                                                                                                                                                                                                                               Score 446; DB 1;
Pred. No. 1.74e-33;
72; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                               Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 778;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                          Gaps 33;
                                              298
244
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Best Local S
Matches 10
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Membrane binding element; thrombotic disease; soluble protein; complement-related disease; integral membrane protein; inflammation; short consensus repeat; SCR 1-3; CRI; complement receptor type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane-binding elements (MBE) of low membrane affinity covalently associated with (I). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (I) itself, specifically inflammation or any other complement-related disorder (e.g. neurological disease, graff rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others; including application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischaemia or asthma and as immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or inhalation at 0.01-10 (preferably of 1-10) memory of the sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1998.
08-JUL-1997; E03715.
15-JUL-1996; GB-014871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W45899 standard; peptide; 1930 AA.
W45899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents human complement receptor 1 (CR1, CD 35) N-terminal fragment. The invention relates to a soluble derivative (A) of a soluble polypeptide (I), which comprises at least 2 heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derivatives of soluble poly:peptide(s) bonded to low affinity membrane binding groups - useful for treating complement-rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 98-110524/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombotic diseases, providing improved localisation at cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ADPR-) ADPROTECH PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Pages 60-61; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                136 FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
253 SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                       189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1-10) mg/kg/day.
equence 1930 AA;
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                                                                                                                                                                                                                                                                                      24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                              22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                     Match 13.2%;
Local Similarity 32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTCEVKSCDDFMGQLLNGRVLF 377
                                                                               IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC 252
                                                                                                                                                                                                       GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                        IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                                                                                                                                 IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                                                                                                                                                                                                                                                                            104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mossakowska DEI, Smith RAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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in W45889"
                                                                                                                                                                                                                                                                                                                                                                            Score 446; DB 1; Length 1930;
Pred. No. 1.74e-33;
72; Mismatches 108; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating complement-related
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01-APR-1988; US-176532.
(TCEL) T Cell Sciences Inc; (UYJO) The Johns Hopkins University; (BRIG*) The Brigham and Women's Hospital.
Fearon DT, Klickstein LB, Wong W, Carson G, Concino MF, Makrides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc Claim 1; fig. 1; 191pp; English. This is full-length CR1 protein, and shortened forms are new, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x=untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (CR) of 6 long direct homologous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and C can detect CR2 sequences. They are useful in diagnosing and treating immune disorders, and preven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; N91477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO8909220-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid sequences encoding new CRI protein - and its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 89-309498/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      perfusion injury.
Sequence 2317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                186 FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 242
                                                                                                                                                                                      243 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                          127 IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 185
300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                                                                                  72 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                      GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                        EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                  EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                      PTCEVKSCDDFMGQLLNGRVLF 381
                                                                                                              SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                                                                                                                            IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%;
Similarity 32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
72; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 446; DB 1; Length 2317; Pred. No. 1.74e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and prevent
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RESULT ID R

T 10 R28553 standard;

peptide;

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Pr Calaim 11; Fig 2 and R11810; 23pp; English.

CC The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

CC 168:1255-1270. It encodes the first 8 and a half amino terminal

CC SCRs of CR1. The invention concerns analogues of "regulator of

CC complement activation" proteins or truncated, hybrid or recombinant

CC complement of them. CR1-4 is a preferred truncated form and a number of

CC specified substitution variants of it are claimed in which certain

CC specified substitution variants of it are claimed in which certain

CC specified of 3bb- and C4b-binding are substituted by amino acids from

CC degree of C3b- and C4b-binding are substituted by amino acids from

CC contain the CR1-4 sequence; the sequence given here was constructed

CC contain the CR1-4 sequence; the sequence having GENESED

CC accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
300 PRCSLKPCD-F-PQFKHGRLYY 319
                                        310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                    189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating auto: immune diseases, to suppress transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atkinson JP, Hour WPI; 92-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
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CR1-4 (85R, 87N) analogue.
Short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
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19-MAR-1993
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                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
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                                                                                                   SRV-COPPPDVLHAERTORDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                   EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                      IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                                                                                                                                                                                         IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                                                                                                                          FIS--TNRE-NFHYGSVYTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                               YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                             GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                            IKGIQFGSRINYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SCR-1
61. .122
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 441; DB 1;
Pred. No. 5.77e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 543;
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                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                                                               VQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or for diagnosis etc.

To for diagnosis etc.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 15; Fig 2 and R11810; 23pp; English.

Claim 16; Fig 2 and R1810; 23pp; English.

Claim 16; Fig 2 and R1810; 23pp; English.

Claim 17; Fig 2 and R1810; 23pp; English.

Complement activation for the green of truncated, hybrid or recombinant of complement activation variants of it are claimed in which certain constitution variants of it are claimed in which certain degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-1992.
28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
300 PRCSLKPCD-F-PQFKHGRLYY 319
                                310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                        189
                                                                                                                                                              193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEDELPSC
                                                                                                                                                                                                                               136 FIS--THRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atkinson JP, Hou: WPI; 92-375009/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28560;
19-MAR-1993 (first er
CR1-4 (114S) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating auto:immune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R28560 standard; peptide; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
                                                                                                                                                                                                                                                                 83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                77 IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWSNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                                                                                                                                                                                                                                    24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                                    22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                           EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                           SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                              EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV
                                                                                                                                                                                                                                                                                                                                                                                                                103;
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Asp substituted by Ser (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= SCR-2
451, .510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 439; DB 1;
Pred. No. 9.31e-33
                                                                                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to suppress transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 108; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.MAR-1993 (first entry)
CR1-4 (109N, 110A, 111A, 112H) analogue.
Short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R28558 standard; peptide; 543 AA. R28558;
                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1992.
28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "Thr substituted by Ala misc_difference 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Asp substituted by Asn (SCR-9)" misc_difference 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                    Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON.
Atkinson JP, Hourcade D, Krych M;
WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference 112
                                                                                 83
                                                                                                      77
                                                                                                                        24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                            22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                    FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                 GSEFEFGAKVVYTCDEGYQLLGE--IDYREC-DADGWINDIPICEVVKC-LPVTELENGR 138
                                                                                                     IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGNAAHWDNETPICDRIPCGLPPT-ITNGD 135
EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                   IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                        IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                                                              Similarity
                                                                                                                                                                                                               543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   303826
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511. .543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note "Ile substituted by His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Val substituted by Ala (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "TRUNCATED"
                                                                                                                                                                             13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .510
                                                                                                                                                                   Score 439; DB 1;
Pred. No. 9.31e-33;
72; Mismatches 109
                                                                                                                                                                     Mismatches 109;
                                                                                                                                                                                         DB 1; Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCR-9)"
                                                                                                                                                                      Indels
                                                                                                                                                                       38;
     244
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Example 8; Page 18 and R11810; 23pp; English.

The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

168:1255-1270. It encodes the first 8 and a half amino terminal

SCRS of CR1. The invention concerns analogues of "regulator of

Complement activation" proteins or truncated, hybrid or recombinant

complement activation proteins or truncated form and a number of

specified substitution variants of it are disclosed in which certain

specified substitution variants of it are disclosed in which certain

positions in SCR-5-6 are substituted by amino acids from

the corresponding positions in SCRs which are involved in C3b-

and

C4b-binding. The substitution variant given here has increased C3b-

the sequence given here was constructed from the CR1-4 sequence;

the sequence given here was constructed from the full-length CR1

amino acid sequence having GENESEQ accession number R11810 and

descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1993 (first entry)
CR1-4 (364-367 NAAH) analogue.
short consensus repeat; regulator of complement activation;
c3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Кеу
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R28571 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1992.
28-APR-1992; 303826.
03-MAY-1991; US-695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atkinson JP, Hourcade D, Krych M; WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating auto:immune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosis etc
                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                        24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV
                                                                                                                                                                                                                                                                                                                                                                                         22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 13.0%;
Local Similarity 31.9%;
les 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTCEVKSCDDFMGQLLNGRVLF 331
                                                                   IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV
                                                                                                  FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                              GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                           IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-IINGD
IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364. .367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "MESL substituted with NAAH from
SCR-8-9 to increase C3b binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SCR-9
/note= "TRUNCATED"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 438; DB 1; Le
Pred. No. 1.18e-32;
79; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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► Db
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT

ACC RESULT
                                                                                                                                                                                                                                                                                                                                                                                                   or diagnosis etc.

Staim 11; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 14; Fig 2 and R11810; English.

Complement activation to concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of composition of them. CR1-4 is a preferred truncated form and a number of compositions in SCR-2 which have been identified as important for the corresponding positions in SCR-9. The specification does not the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Atkinson JP, Houre WPI; 92-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1992.
28-APR-1992; 303826.
03-MAY-1991; US-6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR1-4 (64K) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R28550;
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83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                      77
                                                                                                                                                  24
                                                                                                                                                                                       22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCKNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 CTVNGWEPEVP-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 GNAAHWNSSVPVC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                           YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRCSLKPCDFPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGF--TTPSQSYWDYLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTCEVKSCD--DFM-GQLL--NGR-VLFPVNLQLGAKVDFVCDEGFQLKGSSASY-CVLA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRY-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA- 299
                                                                                                                                                                                                                                                                       l Similarity
103; Conser
                                                                                                                                                                                                                                                                                                                                                                                                543 AA;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-695514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
511. .54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Arg substituted by Lys (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label=
                                                                                                                                                                                                                                                                                               13.0%;
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.543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCR-9
                                                                                                                                                                                                                                                                 Score 437; DB 1;
Pred. No. 1.50e-32;
72; Mismatches 109
                                                                                                                                                                                                                                                       Mismatches 109; Indels 38;
                                                                                                                                                                                                                                                                                                                         Length 543;
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δÃ В Ş 밁

Ω

В

461 FPIGTSLKYECRPEYYGR-PFSITCLD-NLVWSSPKDVCKRKSCKTPPD-PVNGM-VHVI 516

106;

Indels 38;

Gaps

24 YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG 83

Matches

Conservative

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В
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                                      Query Match
                                                                                                        damage due to inflammation and in treatment of thrombosis Disclosure; Fig 5; 234pp; English.

This sequence comprises three of the four tandem, direct, long homologous repeats of the full-length F allozyme of CR1. LHR-A is absent. Each LHR might represent a single C3b/C4b binding domain, making the receptor multivalent. The LHR's are composed of 7 short consensus repeats of 60-70 residues resembling the SCR's of other c3/C4 binding proteins. The protein and fragments of it having C3) and/or C4b binding activity can be used to treat immune disorders
                                                                  Sequence
                                                                                          or disorders involving inappropriate complement activity.
                                                                                     See also Q11642.
                                                                                                                                                                                                                                                                                                                              (TCEL-) T CELL SCI INC.
(UTGO) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
FEATON DT, Klickstein LB, Wong WW, Carson GR, Hoh M, Concino Makrides SC, Marsh HC;
                                                                                                                                                                                                                                                          Human complement receptor type 1 gene, encoded proteins and fragments – for treatment of immune disorders, myocardial infarct,
                                                                                                                                                                                                                                                                                                       N-PSDB; Q11643
                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-1991.
25-SEP-1990; U05454.
26-SEP-1989; US-412745.
26-SEP-1990; US-912349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response; long homologous repeat; LHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Partial human complement type 1 receptor. complement system; C3b/C4b receptor; CR1; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1991 (
Partial human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R11982 standard; Protein; 1537 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R11982;
                 Match 13.0%;
Local Similarity 32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                     91-132854/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                    1537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1521. .1526
/note= "has 67 per cent homology to site kinase C phosphorylation in the EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1495. .1498
/note= "positively-charged; preceded by hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= LHR-B
439. .891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= LHR-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= LHR-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1341
Score 439; DB 1;
Pred. No. 9.31e-33;
73; Mismatches 106
                           Length 1537;
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Search completed: Thu Jun 8 21:49:27 2000 Job time : 17 secs.
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300 PRCSLKPCD-F-PQFKHGRLYY 319
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Tabular output not generated. Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd >US-09-316-163-14 (1-428) from US09316163.pep 3371 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428 Thu Jun 8 21:49:45 2000; MasPar time 24.14 Seconds 836.361 Million cell updates/sec

Description: Perfect Score:

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: MidImum Match 0%

Histing first 45 summaries Database: pir62 1:pip1 2:pir2 3:pir3 4:pir4

Statistics: Mean 45.494; Variance 73.749; scale 0.617

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21	20	19	18	17	16	. 15	14	13	12	11	10	Q	œ	7		Մ	4	ω	N	1	Result
434	435	446	446	449	. 449	447	470	474	494	537	564	646	683	790	1129	1136	1720	2389	2396	2834	Score
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330	327	2489	2039	2014	661	343	676	. 610	558	597	597	. 331	1053	808	303	452	669	449	1231	1234	Length
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156100	A40455	173012	A28507	I36936	136937	G35070	A45900	I46001	S57953	NBHUC4	S53711	A45222	S46199	D35069	H35068	A35068	S65551	NBHUHS	NBHUH	HSMBN	ID
1	factor H	7	complement C3b/C4b re		complement receptor 1	apolipoprotein H-rela	complement C3b recept	C4b-binding protein a	C4BP protein alpha ch	C4b-binding protein a	C4BP alpha chain prec	complement factor H-r	probable complement r	complement factor H-r	apolipoprotein H-rela	complement factor H-r	H - bovine (ı	complement factor H p	Description
.17e-	.82e-		4.04e-77	7.60e-78	7.60e-78	2.31e-77	6.17e-83	6.57e-84			.53e-	.32e-12	.28e-13					0.00e+00	0.00e+00	0.00e+00	Pred. No.
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cofactor cofactor	<pre>coagulation factor XI membrane cofactor pro</pre>	endothelial leukocyte	E-selectin precursor		apolipoprotein H prec		complement control pr	P-selectin precursor	P-selectin - rat	apolipoprotein H prec	P-selectin precursor	apolipoprotein H homo	complement C3b/C4b re	complement regulatory	sperm-egg recognition	hypothetical protein	complement factor H-r		
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ALIGNMENTS

convertase) in the alternative complement pathway.	C C C C C C C C C C C C C C C C C C C
Factor H functions as a cofactor in the inactivation of dissociation serine proteinase I and also increases the rate of dissociation of the complex (C3 convertese) and the (C3b)nBb complex (C5	COMMENT Fac
Two codominant alleles of factor H are present in mice.	COMMENT Two
#cross-references GB:J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926	##CTOSS-
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Dexamethasone and IFN-gamma increase the level of h in	
h 1	#title
Biochemistry (1989) 28:9891-9897	#journal
Minoz-Canoves, P.: Tack, B.F.: Vik, D.P.	######################################
##Cross-references GB:M31979; NID:g193/26; P1DN:AAA3//62.1; F1D:g193/29	##Cross-:
1-18 ##label RES	##residues
	##molecule_type
<pre>preliminary; translated from GB/EMBL/DDBJ</pre>	
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H by the complete cDNA sequence of the H.2 allotype: #cross-references MUID:90111033	#cross-refe
9	#title
J. Immunol. (1990) 144:358-362	#journal
Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y.	#authors
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ein H is comprised	#title
(1986) 83:3963-3967	#journal
nsen, T.; Tack, B.F.	#authors
A26154; I49711; I49728 A26154	ACCESSIONS REFERENCE
30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999	DATE
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complement factor H precursor - mouse	TITLE
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1030,1061,1225
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509-564
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178-205,210-251,
237-262,267-309,
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121 PICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLW 180
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                                                                                                                                                                                    Local Similarity 83.0%; nes 356; Conservation
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                             PLCEVVKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLW 198
                                                            ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDI 120
                                                                                                                                          EDCKGPPPRENSEILSGSWSEQLYPEGTQATYKCRPGYRTLGTIVKVCKNGKWVASNPSR 78
                                                                               ICRKKPCGHPGDTPFGSFRLAVGSQFEFGAKVVYTCDDGYQLLGEIDYRECGADGWINDI 138
                                                                                                                        EDCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSR 60
                                                                                                                                                                                                                                                 #length 1234 #molecular-weight 139081 #checksum 3676
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T.J.R.; Sim, R.B.
#journal Biosci. Rep. (1987) 7:201-207
#title Sequence analysis of a cDNA clone encoding the C-terminal end
#cross-references MUID:88025472
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#journal Eur. J. Immunol. (1991) 21:799-802
#title Human complement factor H: two factor H proteins are derived
#cross-references moil: #cross-references moil:
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##cross-references EMBL:Y00716; NID:g31964; PIDN:CAA68704.1; PID:g31965
##note 402-Tyr was also found
##note parts of this sequence, including the amino and carboxyl
ends of the mature protein, were confirmed by protein
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Ripoche, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbe R.D.; Sim, R.B.
Biosci. Rep. (1986) 6:65-72
Partial characterization of human complement factor H by
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#journal Biochem. J. (1982) 205:285-293
#title Purification and structural studies on the complement-system control protein beta-1-H (factor H).
#cross-references_MUID:83048213
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#accession A61565
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#title Cloning of the 1.4-kb mRNA species of human complement factor
H reveals a novel member of the short consensus repeat
family related to the carboxy terminal of the classical
150-kDa molecule.
#cross-references MUID:91201892
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#journal Biochin. Biophys. Acta (1996) 1289:305-311
#title Factor H co-purifies with thrombospondin isolated from platelet secretate.
#cross-references_MIID:96205365
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                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type protein
##residues 411-419;574-578,580-582 ##label CAR
# Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
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                                                                                                                                                                                                                             ##cross-references GDB:120041; OMIM:134370
                                                                                                                                                                                                                                                                                                         in repeat 4.
Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver. See also PIR:NBHUHS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.; Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D. Biochemistry (1992) 31:3626-3634 Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Mol. Biol. (1991) 219:717-725
Three-dimensional structure of a complement control protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotation; NMR structure determination, residues 264-292
the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have several allelic forms
                                                                                                                                                                                                                                                     GDB:HF1; HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S66298
                                                                                                                                               GDB:HF2; HF
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            y Match 71.1%;
Local Similarity 67.5%;
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            Score 2396; DB 1; Length 1231; Pred. No. 0.00e+00;
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##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492;
PIDN:CAA30403.1; PID:g758073
##note part of this sequence, including the amino end of the mature protein was confirmed by protein sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPSCEEKSCDNPYIPNGDYSPLRIKHRIGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNEKPQCVEISCLPPRVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPRCIRVK 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDI 120
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Eur. J. Immunol. (1986) 16:1351-1355
Human complement factor H: isolation of cDNA clones and partial cDNA sequence of the 38-kDa tryptic fragment containing the binding site for C3b.
                                                                                                                                                                                                                                                                                                       Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts.
                                                                                                                    Schulz, T.F.; Schwaeble, W.; Stanley, K.K.;
                                                                                                                                                                                                                                                                         в60238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement factor H precursor, short splice form - human complement factor H-related protein; complement protein H #formal_name Homo sapiens #common_name man 31-Dec-1993 *sequence_revision 23-Feb-1996 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete amino acid sequence of human complement factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B. Biochem. J. (1988) 249:593-602
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                                                                                                   Dierich, M.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-Jun-1999
                                                                                                                                                              1-33#434-449 ##label EST
only portions of this 1.8 kilobase mRNA were sequenced
                                                                                                                                                                                                                                         not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                   402-Tyr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #type complete
                                                                                                                    Weiss, E.;
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CLASSIFICATION
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#title
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Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-3634

#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
                                                                                                                                                                    #description
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Dierich, M.P.; Weiss, E.H.
#journal Eur. Immunol. (1987) 17:1485-1489
#title Human complement factor H: expression of an additional truncated gene product of 43 kDa in human liver.
#cross-references_MUID:88055295
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#accession A27877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 226-401,'Y',403-449 ##label KRI ##cross-references GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473 Factor H has also been found bound to cell membranes in an unknown manner. However, it has at least one cell attachment site motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
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Alternative
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                                      a cofactor in the inactivation of C3b by serine proteinase also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
 \hbox{\tt\#superfamily complement factor H; complement factor H repeathomology } 
                                                                                                                                                                                                                                     the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have
                                                                                                                                                                                                                                                                                                                                                                 GDB:HF2; HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structural analysis of human complement protein H: homology with C4b binding protein, beta(2)-glycoprotein I, and the Ba fragment of B.
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J. Immunol. (1986) 136:3407-3411
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Sim, R.B.; Discipio, R.G.
Biochem. J. (1982) 205:285-293
Purification and structural studies on the complement-system
control protein beta-1-H (factor H).
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114-141,146-192,

178-205,210-251,

237-262,267-309,

294-320,325-374,

357-385,389-431,
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                   #journal
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                                                                                                                                                                                                                                           PPKCVRI 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 449 #molecular-weight 51007 #checksum 6077
Soames, C.J.; Day, A.J.; Sim, R.B.
Biochem. J. (1996) 315:523-531
Prediction from sequence comparisons of residues of factor H
                                                                                                           #formal_name Bos primigenius taurus #common_name cattle 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
                                                                                                                                                 s65551 #type fragment
factor H - bovine (fragment)
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#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
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64; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 449;
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Best Local :
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355-412
416-471
476-530
538-592
599-651
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  86-146
150-203
                                                                                                                                                                                                                                                                                                                                                                                                     #authors
                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                              #cross-references MUID:90153969
                                                    28-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-669 ##label SOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 NGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 NGVYRPELSKYRGQDKITYECKKGFFPEIRGTDATCTRDGWVPVPRCAWKPCSYPVIKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 RVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIP
                                                                                                                                                    ##residues 1-452 ##label VIK
##cross-references GB:M29010; NID:g192561; PIDN:AAA37415.1; PID:g387128
##note translation of the nucleotide sequence is not complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 VEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 LENGHNOHREEKYLQGETVRVHCYEGYSLQNDQNTMTCTESGWSPPPRCIRVK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 GSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDIPICEVVKCLPVTELE 135
                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GSPHLAEGNQFEYGAKVVYTCDEGYQMYGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLYY--SYRGYFPARVNOOFVYSCDHHFVPPSQRSWDHLACTAEGWSPEEPCLROCIFNY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCIFHY
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Similarity 58.4%;
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                                                                                                                         translation of the nucleotide sequence is not complete *superfamily complement factor H; complement factor H repeat
                                                                                                                                                                                                                                                         A35068
                                                                                                                                                                                                                                                                                                        B.F.; Chaplin, D.D.
J. Biol. Chem. (1990) 265:3193-3201
Identification and sequence analysis of four cfactor H-related transcripts in mouse liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A35068; B35068; C35068; D35068; E35068; F35068; G35068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Mus musculus #common_name house mouse
27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement factor H-related protein 3A4/5G4 - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                        Vik, D.P.; Munoz-Canoves, P.; Kozono, H.; Martin, L.G.;
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                                                                                                       Tomology
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#domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #type fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1720; DB 2;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                sequence analysis of four complement
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FHR4\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal J. Biol. Chem. (1990) 265:3193-3201
#title Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
#cross-references MUID:90153969
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194 ENGWSPPPKCIRIN 207
                                                                                                        296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSY-WDYL 354
                                                                                                                                                                                      236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                            75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPS-GYSWDYL 133
                                                                                                                                                                                                            15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-303 ##label VIK
##cross-references GB:M29007; NID:g192557; PID:g309164; GB:J05259
##note translation of the nucleotide sequence is not complete
FICATION #superfamily complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                               RCTAQGWEPEVPCVRKCVFHYVENGDSTYWEKIYVQGQSLKVQCYNGYSLQNGQDTMTCT 193
                         RCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCTAQGWEPEVPCVRKCVFHYVENGDSAYWEKIYVQGQSLKVQCYNGYSLQNGQDIMTCT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFFVSIGNKYSYRCDNGFSPPS-GYSWDYL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGWSPPPKCVRIK 428
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                                                                                                                                                                                                                                                                                                 33.5%;
Similarity 70.6%;
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Similarity 71.1%;
                                                                                                                                                                                                                                                                                                                                                            #length 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 duplication
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apollipoprotein H-related protein 23L1 - mouse
#formal_name Mus musculus #common_name house mouse
27.Jul-1990 #sequence_revision 31-Dec-1993 #text_change
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                                                                                                                                                                                                                                                                                  Conservative
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#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04
gth 303 #molecular-weight 34498 #checksum 2835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
                                                                                                                                                                                                                                                                              Pred.
24;
                                                                                                                                                                                                                                                                                             Score 1129; DB 2;
Pred. No. 3.28e-249;
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22; Mismatches
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                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                      413 CTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                  353 YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYY 412
                                                                                                                                                                                                                                                                                                         134 CTENGWSPPPKCIRIK 149
                                                                                                                                                                                                                                                                                                                                                                                                             293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                      74 YLRCTVQGWKPEVPCVRKCVFHYVENGEFAYWEKIYVQGQSLKVQCYNGYSLQNGQDTMT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LTAWLSTAKGEVKSCEFPQFKYGRLYFEEILRPNFPVSIGNKYSYKCDNGFSPPSGLFWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references GB:M29009; NID:g192563; PIDN:AAA37416.1; PID:g309166;
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##residues 1-80
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Dahmen, A.; Kaidoh, T.; Zipfel, P.F.; Gigli, I.
Biochem. J. (1994) 301:391-397
Cloning and characterization of a cDNA representing
                                                                                                             #formal_name Parablax neblifer #common_name barred sand bass
19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change
                                                                                  S46199; S77894
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                                                                                                                                                                  probable complement regulatory plasma protein SB1 - barred
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J. Biol. Chem. (1990) 265:3193-3201
Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
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Pred. No. 1.40e-162;
24; Mismatches 22;
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to human complement factor H. #cross-references MUID:93155112
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                                                                                                  #authors
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##residues 526-532,'x',534-537;809-817,'x',819-826 ##label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 NDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQVIGG 164
                                                                                                                                                                                                                                                                                                                     374 HYVEYGESSYWQRR-YIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 --PEEAT-FGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIENGNV 221
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Local Similarity 31.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG 83
                                                                                                                                                                                                                                                                                                                                                       ENIQDAVIVGTDKQIYNLNQKAIYACGEG-N--RGRITLTCGENGWSGDRKCT-VK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                   VDSWDVRSWERY - - - TLDDNTRYWCKRGYKRTGGVIWA - - TCGRNGWMPNPLCEVKTCSK 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYLKPVYKENERFQYKCKQGFVYKERGDA-VCTG--SGWNPQPSCEEMTCLTPYIPNGIY
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                                      J. Biol. Chem. (1993) 268:2904-2908
A novel short consensus repeat-conta
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30-Sep-1963 #sequence_revision 30-Sep-1993
                                                                                                Skerka, C.; Kuhn, S.; Gunther, K.; Lingelbach,
                                                                                                                                       A45222; S29609
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#journal Biochim. Biophys. Acta (1995) 1261:285-289
#title cDNA structure of rabbit C4b-binding protein alpha-chain.

Preserved sequence motive in complement regulatory protein modules which bind C4b.
#cross-references MUID:95226458
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##cross-references EMBL:X68679; NID:g30869; PID:g30870
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##residues 1-597 ##label MA1
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Local Similarity 31.8%;
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Lintin, S.J.; Lewin, A.R.; Reid, K.B.M.

FEBS Lett. (1988) 232:328-332

Derivation of the sequence of the signal peptide in human C4b-binding protein and interspecies cross-hybridisation the C4bp cDNA sequence.
A90326
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Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C4b-binding protein alpha chain precursor - human C4BP; proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       A33568
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13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change
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                               although the sequence determined extends to residue
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                                                                                                                                                                                                                                                                                                                                       the authors translated the codon
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              above, these authors assign Met-17 as the initiator
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                                                                                                                                                                                                                                                                                                                                                 #authors Suzuki, K.; Nishioka, J.
#journal J. Biol. Chem. (1988) 263:17034-17039
#title Binding site for vitamin K-dependent protein S on complement
#C1b-binding protein.
#cross-references_MUID:89034204
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#title
                                                                       #cross-references MUID:83221615
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Hackeng, T.M.; Iwanaga, S.; Bouma, B.N.

#journal FEBS Lett. (1993) 317:228-232

#title The region Ser(333)-Arg(356) of the alpha-chain of human C4b-binding protein is involved in the binding of complement C4b.

#cross-references_MUID:93146164
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N-terminal sequence analysis and alignment of the fragments
produced by limited proteolysis with chymotrypsin and the
peptides produced by cyanogen bromide treatment.

#cross-references_MUID:85296001
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##residues 381-404 ##label HES
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##residues 49-81 ##label CH1
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##note 92-Thr and 357-His
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                  annotation; electron microscopy; three-dimensional structure;
    ligand binding
                                                                                                               Proc. Natl. Acad. Sci. U.S.A. (1983) 80:3461-3465
Visualization of human C4b-binding protein and its complexe:
with vitamin K-dependent protein S and complement protein
                                                                                                                                                                                                                                                                                                                                 A31785
I52244
                                                                                                                                                                                         Dahlback, B.; Smith, C.A.; Muller-Eberhard, H.J
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Structure of the gene coding for the alpha polypeptide chain
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Blochem. J. (1985) 230:133-141
Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.
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#cross-references MUID:91113199
#accession I52244
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NT C4BP controls the classical pathway of complement activation. It
binds as a cofactor to C3b/C4b inactivator (C3bINA), which then
hydrolyzes the complement fragment C4b. It also accelerates the
degradation of the C4bC2a complex (C3 convertase) by dissociating
the complement fragment C2a.

NT C4BP occurs in plasma in two forms, both of which bind complement
fragment C4b. The prevalent higher molecular weight form contains
7 alpha chains and one beta chain, which are linked by disulfide
bonds. The beta chain binds the vitamin K-dependent plasma
protein S. A minor form lacks the beta chain. Bound protein S is
inactive as a cofactor for protein C inactivation of coagulation
factors V and VIII.
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ap_position 1q32-1q32
ntrons 48/1; 110/1; 143/2; 172/1; 236/
        176
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                                                                                         219
                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 15.9%;
Local Similarity 30.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 NC-GPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNP 58
    -EN---GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD 230
                                                                                     VENETIGVWRPSPPTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSV 278
                                                                                                                                                                      WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
                                                                                                                                                                                                                                                    WSHPLPQCEIVKCKPPPDIRNGR-HSG--E-ENFYAYGFSVTYSCDPRFSLLGHASISCT 218
                                                                                                                                                                                                                                                                                                                                     SRICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYR-EC-DAD-G 115
                                                                                                                                                                                                                                                                                                                                                                                                                  FCIY-KR-CRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The molecule has a central body supporting seven tentacles (alpha chains), each with the binding site for C4b at the peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute phase; chylomicron; complement pathway; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           octamer of seven alpha chains and one beta chain 
#superfamily C4b-binding protein alpha chain; con 
factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain complement factor H repeat homology *label #domain complement factor H repeat homology *label #region complement C4b binding #status predicted\
#domain complement factor H repeat homology *label #label #labe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #product C4b-binding protein alpha chain
predicted #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110/1; 143/2; 172/1; 236/1; 297/1; 362/1; 425/1; 482/1;
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1597 #molec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #molecular-weight 67033 #checksum 6374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 537; DB 1; Le
Pred. No. 2.52e-99;
85; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasma
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390-443
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PID: g899380
FICATION #superfamily C4b-binding protein alpha chain; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 EISFSCHETSRFSAI-CQGDGTWSPRTPSCGDICNFP-PKIAHGHYKQSSSYSFFKEEII 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AVC-TGSGWNP-QPSCEEMTCLT-PYIPNGIY-T-PHRIKHRI--DDEI-RYECKNGFYP 282
   231 AVCTGSG-WNPQPSCEEMTCL-TPYIPNG--IYTPH-RIKH--RIDDEIRYECKNGFYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%;
Local Similarity 29.5%;
hes 132; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 C-GPPP-DLPYALPASEMNQTDFESHTTLRYNCRPGYSRASSSQSLYCKPLGKW-QINIA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 --CVKKSCRNPGDLQNG--KVEVKTDFLFGSQIEFSCSEGYILIGSSTSYCEIQGKGVSW 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QCHSGYSLPNGQDTYYCTENGWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTDEPTTVICQKNLRWTPYQGCEALCCPEPKLNNGEIT-QH-RKS-RPANHC-VY-FYGD 393
                                                                                                                                                                                                                        VVNKTVGVWSPSPPTCERIICPWPKVLHGTINSGFKHTYKYKDSVRFVCQKGFVLRGSGV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGE-IDYRECDADG--W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKGPPPRENSEILSGSWSEQL-YSEGTQATYKCRPGY-RTLGTIVKVCKN-GEWVPSNPS
                                                                         IHCEADGSWSPVPVCELNSCTDIPDIPNAALITSPRPRKEDVYPVGTVLRYICRPGYEPA 303
                                                                                                                                                  E-N---GLWSNEKPQCVEISCLPPRVENGD-GIYLKPVYKENERFQYKCKQGFVYKERGD
                                                                                                                                                                                                                                                                                                 TNDIPICEVVKC-LPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
                                                                                                                                                                                                                                                                                                                                                                       SDPLPECVIAKCGMP-PDISNGK-HNGR-E-EEFFTYRSSVTYKCDPDFTLLGNASITCT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillarp, A.; Thern, A.; Dahlback, B. submitted to the EMBL Data Library, July 1995 Molecular cloning of rat C4b-binding protein alpha- and beta-chains: structural and functional relationships human, bovine, rabbit, mouse and rat proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S57953
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C4BP protein alpha chain precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
13-Jan-1996  #sequence_revision 01-Mar-1996  #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length 558
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Pred. No. 8.78e-89;
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362 CKEVCCPEPNLNNYGSITLH--RRP----STSTHCTYISGDKISYECHSKYMFDAL-CTK 414
                                                                                                                                                                                                              302 LPHIPHALWERYDHQTQTEQQVYDIGFVLSYKCHFGYKPETDGPTTVTCQSNLEWSPYIE 361
                                                                                                              252 -PYIPNGI---YTPH-RIKHRI-DDE-I-RYECKNGFYPATRSPVS-KC-TITGWIPAPR
                                                                                                                                                                                                                                                                                              195 PRVENGDGIY-LKPYYKENERFQYKCKQGFYYKERGDAVC-TGSGWNPQP-SCEEMTCLT 251
                                                                                                                                                                                                                                                                                                                                                                             242 PVVKDGKITSGFGPIYTYQQSIVYACNKGFRLEGDSLIHCEADNSWNPPPPTCELNGCLG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 IVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS-EN---GLWSNEKPQCVEISCLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 -HNGGDE-DF-YTYGSSVTYSCDRDFSMLGKASISCRVENKTIGVWSPSPPSCKKVICVQ 241
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PID:g469118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 14.1%;
Local Similarity 27.9%;
les 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGSEFEFGAKVVYTCDEGYQLLGEID-YRECDADG--WTNDIPICEVVKCLPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSEGTQATYKCRPGYRTLG-TIVKVCKNGE-WVPSNPSRICRKRPCGHPGDTPFGSFRLA 81
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J. Immunol. (1994) 153:4190-4199
Bovine C4b binding protein. Molecular cloning of the alpha-
and beta-chains provides structural background for lack of
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Best Local Similarity 31.7%;
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INCE I48306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 CSLKPCDFPQFKH-GRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQS-Y-WDYLRCTV 358
              99 G--IEFGSTITYSCNQGYRLIGDSSATCIVSDNTVMWDNDMPLCESIPCESPPAISNGDF 156
                                                         24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                          42 FAIGTTWEYKCRPGYFRKSFIIT-CLETSKW--SDAQQFCKRKPCMNPQEPLHGSVHINT 98
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                                                                                                                                          101;
  Wagner, L.M.; Holers, V.M.

J. Exp. Med. (1995) 181:151-159

Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of both human decay-accelerating and membrane cofactor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #formal_name Mus musculus #common_name house mouse
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. (1990) 144:3581-3591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement C3b receptor type 2 long form precursor - mouse
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                                                                                                                                      72;
                                                                                                                                                      Score 470; DB 2;
Pred. No. 6.17e-83;
                                                                                                                                      Mismatches 111; Indels
Length 676;
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Best Local Similarity 41.4%;
Matches 55; Conservative
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92-145
154-208
215-269
273-334
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#journal J. Biol. Chem. (1990) 265:3193-3201
#title Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
#cross-references MUID:90153969
                                                                                                                                                                           353 YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYY 412
                                                                                                                                      134 CAEEGWSITPKCI 146
                                                                                                                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-343 ##label VIK
##cross-references GB:M29008; NID:g192559; PID:g309165; GB:J05259
##note translation of the nucleotide sequence is not complete
#FICATION #superfamily complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 F-MGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNTVPT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 -ISCLPPRVENG--DGIYLKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQ-PSC 244
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##residues
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                                                                                          CTENGWSPPPKCV 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH5
#domain complement factor H repeat homology #label FH5
#length 343 #molecular-weight 38443 #checksum 9901
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apolipoprotein H-related protein 13G1 - mouse
#formal_name Mus musculus #common_name house mouse
27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change
10-Sep-1997
G35070; A35071; B35071; H35070; I35070
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:50:30 2000; MasPar time 15.22 Seconds 856.639 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-316-163-14 (1-428) from US09316163.pep 3371 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428

Scoring table: PAM 150 Gap 11

Post-processing: Minimum/Match 0% Listing first 45 Searched: 83857 seqs/ 30454973 residues gummaries

Database: swiss/prot38 1:swissprot

Statistics: 46.246; Variance 66.763; scale 0.693

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match 1	Length I	BB	ID	Description	Pred. No.
1	2834	84.1	1234	- ;	CFAH_MOUSE	COMPLEMENT FACTOR H PR	0.00e+00
N	2396	71.1	1231	Н	CFAH_HUMAN	COMPLEMENT FACTOR H PR	0.00e+00
w	646	19.2	331	μ	CFHD_HUMAN	COMPLEMENT FACTOR H-LI	8.26e-142
4	537	15.9	597	ш	C4BP_HUMAN	C4B-BINDING PROTEIN AL	1.67e-111
σı	494	14.7	558	Н	C4BP_RAT	C4B-BINDING PROTEIN AL	1.09e-99
თ	474	14.1	610	\mathbf{L}	C4BP_BOVIN	C4B-BINDING PROTEIN AL	3.15e-94
7	446	13.2	2039	۳	CR1_HUMAN	COMPLEMENT RECEPTOR TY	1.27e-86
œ	434		330	Н	CFH1_HUMAN	COMPLEMENT FACTOR H-LI	2.23e-83
9	434	12.9	469	۳	C4BP_MOUSE	C4B-BINDING PROTEIN PR	2.23e-83
10	431	12.8	270	-	CFHE_HUMAN	COMPLEMENT FACTOR H-LI	1.44e-82
11	396	11.7	263	۳	VCP_VACCV	COMPLEMENT CONTROL PRO	3.54e-73
12	390	11.6	830	ب	LEM3_HUMAN	P-SELECTIN PRECURSOR (1.41e-71
13	375	11.1	345	<u>س</u> و	APOH_MOUSE	BETA-2-GLYCOPROTEIN I	1.37e-67
14	374	11.1	768	<u>س</u>	LEM3_RAT	P-SELECTIN PRECURSOR (2.51e-67
15	367	10.9	345	H	APOH_HUMAN	BETA-2-GLYCOPROTEIN I	1.79e-65
16	368	10.9	768	1	LEM3_MOUSE	P-SELECTIN PRECURSOR (9.73e-66
17	364	10.8	345	Н	APOH_CANFA	BETA-2-GLYCOPROTEIN I	1.11e-64
18	357	10.6	610	μ	LEM2_HUMAN	E-SELECTIN PRECURSOR (7.76e-63
19	359	10.6	612	ب	LEM2_MOUSE	E-SELECTIN PRECURSOR (2.31e-63
20	348	10.3	668	Н	F13B_MOUSE	COAGULATION FACTOR XII	1.80e-60
21	345	10.2	377	ب	MCP_HUMAN	MEMBRANE COFACTOR PROT	1.10e-59
22	344	10.2	1025	_	CR2_MOUSE	COMPLEMENT RECEPTOR TY	2.01e-59
23	341	10.1	345	\vdash	APOH_BOVIN	BETA-2-GLYCOPROTEIN I	1.236-30

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45	4.4	43	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	28	27	26	25	24	
225	226	226	232	255	268	274	276	291	292	294	301	304	306	309	313	323	328	327	328	329	335	
6.7	6.7	6.7	6.9	7.6	8.0	8.1	8.2	8 6	8.7	8.7	8.9	9.0	9.1	9.2	9.3	9.6	9.7	9.7	9.7	9.8	9.9	
372	372	372	372	1019	646	360	407	390	549	340	485	611	1033	297	381	484	958	661	507	551	769	
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LEM1_RAT	LEM1 MACMU	LEM1_PAPHA	LEM1_MOUSE	LFC_TACTR	LEM3_BOVIN	CCPH_HSVSA	DAF2_MOUSE	DAF1_MOUSE	LEM2_RAT	DAF_PONPY	LEM2_BOVIN	LEM2_CANFA	CR2_HUMAN	APOH_RAT	DAF_HUMAN	LEM2_PIG	HIG_DROME	F13B_HUMAN	DAF_CAVPO	LEM2_RABIT	LEM3_SHEEP	
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2.60e-29	1.49e-29	1.49e-29	5.24e-31	1.15e-35	o. ble-40	2.05e-41	5.42E-42	1.ULE-45	5.61e-46	1./30-45	2.81e-46	4.//e-49	1.456-49	2.4/e-50	2.30e-51	5.9/e-54	3.00e-55		3.00e-33	1.600-00	4.52e-57	

ALIGNMENTS

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0 ct i= ct		TAH_MOUSE STANDARD; PRT; 1234 AA. 06909; 1-JAN-1988 (Rel. 06, Created) 1-JAN-1988 (Rel. 06, Last sequence update) 1-JAN-1988 (Rel. 06, Last sequence update) 1-JAN-1988 (Rel. 05, Last annotation update) 10.MPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1-H). 11. Standard (Mouse). 12. Standard (PROTEIN BETA-1-H). 13. Sciurognathi; Muridae; Murinae; Mus. 14. Sciurognathi; Muridae; Mus. 15. Sciurognathi; Muridae; Mus. 16. Sciurognathi; Muridae; Mus. 17. Tack B.F.;

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license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).
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Best Local
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SEQUENCE OF 53-445 FROM N.A. MEDLINE; 87054207.

SCHULZ T.F., Schwaeble W., St. "Human complement factor H: i. sequence of the 38-kDa tryptifor C3b.";
                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
COMPLEMENT FACTOR H PRECURSOR.
HF1 OR HF OR CFH.
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 MEDLINE; 88134059.

Ripoche J., Day A.J., Harris T.J.R.,

"The complete amino acid sequence of
Biochem. J. 249:593-602(1988).
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TISSUE=LIVER;
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"Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-glycoprotein I, and the Ba fragment of B2.";
J. Immunol. 136:3407-3411(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Solution structure of a pair magnetic resonance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J., Driscoll P.C., Sim B., Campbell I.D.;
"Solution structure of the fifth repeat of factor H: a second example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91278097.

Norman D.G., Barlow P.N., Baron M., Day A.J., Sim B., Campbell I.D.

"Three-dimensional structure of a complement control protein module
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Barlow P.N., Steinkasserer A., Norman D.G., Kieffer B.,
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FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION OF C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF THE C3B BY COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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  TISSUE=LIVER;
MEDLINE; 93155112.
Skerka C., Kuehn S.,
                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                    Eutheria; Primates; Catarrhini; Hominidae; Homo
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Similarity 67.5%;
289; Conservative
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                                                                                                                     Chordata; Craniata; Vertebrata; Mammalia;
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    Guenther K.,
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/FITIG=VAR_001979.
C -> Q (IN REF. 3).
T -> V (IN REF. 3).
T -> Q (IN REF. 3).
RP -> IL (IN REF. 2).
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Pred. No. 0.00e+00;
Lingelbach K.,
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Zipfel
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                                                                                                                                                                                                                                                                  P04003;
P044003;
P044
                 Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;
"Molecular cloning of the cDNA coding for proline rich
identity of PRP as C4b-binding protein ",
Biochem. Biophys. Res. Commun. 165:138-144(1989).
                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 MEDLINE; 90073699.
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CARBOHYD
                                                                                                                                                              SEQUENCE FROM N.A.
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REPEAT
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                                                                                                                                          TISSUE=LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel short consensus repeat-containing molecule is related human complement factor H.";
J. Biol. Chem. 268:2904-2908(1993).
-i- FUNCTION: MIGHT BE INVOLVED IN COMPLEMENT REGULATION.
-i- SUBCELLULAR LOCATION: EXTRACELLULAR.
-i- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
-i- SIMILARITY: STRONG, TO FACTOR H.
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llarity 56.3%;
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26; Mismatches
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Pred. No. 8.26e-142;
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SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
POTENTIAL.
POTENTIAL.
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5 X SUSHI (SCR) REPEATS.
SUSHI 1.
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POTENTIAL.
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165:138-144(1989).
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                                                            protein (PRP):
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Dahlback B., Smith C.A., Mueller-Eberhard H.J.;

Dahlback B., Smith C.A., Mueller-Eberhard H.J.;

Wisualization of human C4b-binding protein and its complexes with

Wrisualization of human C4b-binding protein for the complexes with

Visualization of human C4b-binding protein and its complexes with

Visualization of human C4b-binding protein for c3b.

Vitamin K-dependent protein S and complement protein C4b. ";

Vitamin K-dependent protein S and complement protein C4b.";

Vitamin K-dependent protein S and complexent Frackent Frackent C4b. IT SC CASINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRACKENT C4B. IT

CC CASINA, WHICH THEN HYDROLYZES THE COMPLEMENT FRACKENT C4B. IT

CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S

CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S

CC -I SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA CHAINS AND BETA CHAINS

CC -I SUBUNIT: DISULFIDE-LINKED COMPLEX OF TALPHA CHAINS AND BETA CHAINS OF A 530 KD HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KD COMPLEX OF G ALPHA CHAINS AND I BETA CHAIN. THE CENTRAL BODY OF THE CHAIN CHAINS AND I BETA CHAIN THE CENTRAL BODY OF THE CHAIN CHAINS AND I BETA CHAIN CHAI
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Lintin S.J., Lewin A.R., Reid K.B.M.;
Lintin S.J., Lewin A.R., Reid K.B.M.;
"Derivation of the sequence of the signal peptide in human
"Derivation of the sequence cross-hybridisation of the C4bp
C4b-binding protein and interspecies cross-hybridisation of the C4bp
CDNA sequence.";
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"Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited proteolysis with chymotrypsin and the peptides produced by cyanogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chung L.P., Bentley D.R., Reid K.B.M.; "Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system."; Biochem. J. 230:133-141(1985).
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EMBL; M31452;
EMBL; M62486;
EMBL; M62475;
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, AND LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., Okamura S.,
                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                       SITE FOR C4B AT THE END.
TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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on of the alpha
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                                            107
116 WINDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
             163 WSHPLPQCEIVKCKPPPDIRNGR-HSG--E-ENFYAYGFSVTYSCDPRFSLLGHASISCT 218
                                                                        49 NC-GPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNT 106
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M62484; AAA36506.1;
M62485; AAA36506.1;
M62485; CAA30701.1;
X07853; CAA30701.1;
X04284; CAB51244.1;
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M62477;
M62478;
M62479;
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X02865; CAA26617.
                             SRICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYR-EC-DAD-G 115
                                           FCIY-KR-CRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVG
                                                          DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNP 58
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                                                                                         138;
                                                                                                Similarity
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AAA36506.
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Pred. No. 1
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/FTId=VAR_001977.
Y -> H
                                                                                         Pred.
85;
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SUSHI
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Y SIMILARITY.
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                                                                                          Mismatches
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BETA CHAIN)
                                                                                                        Length 597;
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A Hillary A., Wiklund H., Thern A., Dahlback B.;

RT "Molecular cloning of rat C4b binding protein alpha- and beta-chains: 
RT "Molecular cloning of rat C4b binding protein alpha- and beta-chains: 
RT mouse, and rat proteins.";

RT mouse, and rat proteins.";

RI JIMMUNOL 158:1315-1323(1997).

CC -!- FUNCTION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

CC (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT 
CC ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 
CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA 
CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S 
CC SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS. 
CC -!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         REPEAT
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                                                                                                            DOMAIN
                                                                                                                                                                                                         EMBL; Z50051; CAA90391.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR. C4BPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4BP_RAT STANDARD; PRT; 558 AA 053514; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VENETIGVWRPSPPTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSV
                                                                                                                                                                                           P10998; 1VVC
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Q28065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 -- CVKKSCRNPGDLQNG--KVEVKTDFLFGSQIEFSCSEGYILIGSSTSYCEIQGKGVSW
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                                                                                                                                                                                                                                                                                                                                                             CEEGYRLV-GEATISCWYSQWTPAAPQC 443
                                                                                                                                                                                                                          -GFTTPSQSYWDYLRCTVNG-WEPEVP-CLRQCIFH-YVEYGESSYWQRRYIEGQSAKVQ
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(Rel. 35
(Rel. 35
PROTEIN
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ilarity 29.5%;
Conservative
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35, Created)
35, Last sequence update)
35, Last annotation updat
IN ALPHA CHAIN PRECURSOR.
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Pred. No. 1.09e-99;
89; Mismatches 18;
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SUSHI 8.
BY SIMILARITY.
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POTENTIAL.
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INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 182; Indels 45;
                                                                                          610
                       update)
                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                               358
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TAGE THE PROPERTY OF THE PROPE

C4BPA.

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Immunol. 153:4190/4199(1994).

J. Immunol. 153:4190/4199(1994).

-I- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.

-I- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Bovine C4b binding protein. Molecular cloning "Bovine C4b sinding protein. Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                         DISULFID
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DOMAIN
                                                                 CARBOHYD
CARBOHYD
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                             CARBOHYD
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                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).

SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z31693; CAA83498.1;
P10998; 1VVC.
PF00084; sushi; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95015909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.ch/announce/
      AA;
                                                                                                                                                                                                                    2390
2412
425
471
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      68886
      WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C48-BINDING PROTEIN ALPHA CHAIN.
8 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Repeat; Sushi; BY SIMILARITY.
                                                                                                            INTERCHAIN INTERCHAIN
                                                                                                                                                       SUSHI
                                                                                                                                                     Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
                                                                                                                                                                                                                                      Y SIMILARITY
      D806B270E8A06B58
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                                                                                                              BETA CHAIN)
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lack of comple
      CRC64;
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                                                                                                              (POTENTIAL).
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Best Local :
                                                                                                                                                                                         SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR1_HUMAN
P17927;
"Identification of a partial cDWA clone for the human receptor for complement fragments C3b/C4b."; proc. Natl. Acad. Sci. U.S.A. 82:7711-7715/1985
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation (C3B/C4B)
                                                                                                                                                                                                                                "Identification of distinct C3b and human C3b/C4b receptor (CR1, CD35) b J. Exp. Med. 168:1699-1717(1988).
                                                                                                       repeating domains that are composed of characteristics of C3/C4 binding proteing. Exp. Med. 165:1095-1112(1987).
                                                                                                                                                                Klickstein L.B.,
Fearon D.T.;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 89035992.
                                                                                                                                                                                                                                                                                                                                                                                        ANTIGEN).
CR1 OR C3BR
                                                 MEDLINE; 86067975.
Wong W.W., Klickstein L.B.,
                                                                                                                                                              Fearon D.
                                                                                                                                                                                                                                                                            Fearon D.T.;
                                                                                                                                                                                                                                                                                       Klickstein L.B.,
                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474
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                                                                                                                                                 Human C3b/C4b receptor (CR1). Demonstration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 120; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGSEFEFGAKVYYTCDEGYQLLGEID-YRECDADG--WINDIPICEVVKCLPVTELENGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKTDYSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVVWSDPLPQCIIAKCEPPPTISNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKEVCCPEPNLNNYGSITLH--RRP----STSTHCTYISGDKISYECHSKYMFDAL-CTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PYIPNGI---YTPH-RIKHRI-DDE-I-RYECKNGFYPATRSPVS-KC-TITGWIPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVVKDGKITSGFGPIYTYQQSIVYACNKGFRLEGDSLIHCEADNSWNPPPPTCELNGCLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS-EN---GLWSNEKPQCVEISCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSEGTQATYKCRPGYRTLG-TIVKVCKNGE-WVPSNPSRICRKRPCGHPGDTPFGSFRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGWSPP-PKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGWSPAVPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSLKPCDFPQFKH-GRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQS-Y-WDYLRCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPHIPHALWERYDHQTQTEQQVYDIGFVLSYKCHFGYKPETDGPTTVTCQSNLEWSPYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQP-SCEEMTCLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -HNGGDE-DF-YTYGSSVTYSCDRDFSMLGKASISCRVENKTIGVWSPSPPSCKKVICVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NG-WEPEVP-CLRQCIFH-YVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGTWSPRTPECRPDCKSPPVIAHGQHKVVSKFFTFDHQAVYECDKGYILVGAKELS-CTS
                                                                             OF 761-783;
                                                                                                                                                                                         87168191
                                                                                                                                                                                                       OF 503-2039
                                                                                                                                                                                                                                                                                                                                               Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                            Wong
                                                                                                                                                                                                                                                                                       Bartow T.J., Miletic V.,
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27.98;
                                                                                                                                                                                                                                                                                                                                               Chordata; C
Catarrhini;
                                                                              831-845 AND
                                                                                                                                                                          W.W.,
                                                                                                                                                                                                         FROM N.A.
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85; N
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Pred. No. 3.15e-94;
                                                                                                                                                                             Smith J.A., Weis J.H.,
                                                                                                                                                                                                                                                                                                                                               Craniata; Ve
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 180;
                                                                                                                      proteins.";
                                                                              1179-1195
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                                                                                                                                                                                                                                                               C4b
                                                                                                                                                                                                                                                4b recognition sites i
deletion mutagenesis.
                                                                                                                                      the short consensus repeats
                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
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                                                                                                                                                                                                                                                                                         Rabson
                                                                                FROM
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                                                                                                                                                                                                                                                                                         L.D.,
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                                                                                                                                                                              Wilson
                                                                                                                                                                                                                                                                                                                                                             Mammalia
                                                                                                                                                                                                                                                                                          Smith J.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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EMBL; M11617; AAA52298.1; -.
EMBL; M11618; AAA52299.1; -.
EMBL; V00816; CAA68755.1; -.
EMBL; X05309; CAA28933.1; -.
EMBL; X05309; CAA28933.1; -.
PIR; A28507; A28507.
PIR; A24748; A24748.
PIR; B24748; B24748.
PIR; B24748; B24748.
PIR; C24748; C24748.
PIR; C38443; S03843.
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MOD_RES
DOMAIN
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-!- SUBGUNIT: MONOMER.
-!- SUBGULIAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- POLYMORPHISM: CR1 IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM.
-!- POLYMORPHISM: CR1 IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM.
-!- MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3

SPECIFICITY.
-!- MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F ALLOTYPE OF CR1.
-!- SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
                                REPEAT
REPEAT
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REPEAT
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                  942
1003
1065
1137
1137
1196
1257
1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sushi;
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1971
1996
2039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group
                            SUSHI A1.
SUSHI A2.
SUSHI A3.
SUSHI A4.
SUSHI A5.
SUSHI A7.
7 X SUSHI B1.
SUSHI B2.
SUSHI B2.
SUSHI B3.
SUSHI B4.
SUSHI B4.
SUSHI B4.
SUSHI B6.
SUSHI B7.
7 X SUSHI B7.
SUSHI C7.
SUSHI C3.
SUSHI C5.
SUSHI C5.
SUSHI C5.
SUSHI C5.
SUSHI C5.
SUSHI C5.
SUSHI C6.
SUSHI C6.
SUSHI C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENT RECEPTOR TYPE 1.
EXTRACELULAR (POTENTIAL).
POTENTIAL.
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15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36).
                                                           MEDLINE; 91201892.
Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.;
Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.;
Cloning of the 1.4-kb mRNA species of human complement factor H
reveals a novel member of the short consensus repeat family related
to the carboxy terminal of the classical 150-kDa molecule.";
J. Immunol. 146:3190-3196(1991).
                                                                                                                                                                         Homo sapiens (Human).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                         Q03591;
01-JUN-1994
                                                                                                                                                                                                                                                                                  CFH1_HUMAN
                                                                                                                                                                     Eutheria; Primates;
                       SEQUENCE OF 4-330 FROM N.A. MEDLINE; 91268081.
                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
Molecular cloning of a human serum protein structurally related to
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                                                                                                                                                                                                                                                                                                                                 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                       PTCEVKSCDDFMGQLLNGRVLF 372
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                                                                                                                                                                                                           OR CFHL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 13.2%;
Similarity 32.3%;
104; Conservative
           C., Horstmann R.D., Zipfel P.F.;
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                                                                                                                                                                        Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B2FD29B6AD3C5EB7 CRC64;
                                                                                                                                                                                                                                                                                     330 AA.
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L.27e-86;
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J. Biol. Chem. 266:12015-12020(1991).
-!- FUNCTION: MIGHT BE INVOLVED IN COMPLEMENT REGULATION.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                             P08607;
01-AUG-1988 (Rel. 0
01-FEB-1994 (Rel. 2
01-NOV-1997 (Rel. 3
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SEQUENCE
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MIM; 134371; -.
PFAM; PF00084; sushi;
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PIR; S14604; S14604.
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                                                                                                                                                                                      C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                                                                                                                                                                   C4BP_MOUSE
                                                                                                                                              Mus musculus (Mouse).
                                                                                                       Eutheria;
                                                                                                                         Eukaryota;
                    Kristensen
                                        SEQUENCE FROM N.A.
MEDLINE; 88024997.
                                                                                                                                                                                                                                                                                                                                                                                    367 CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307
cDNA structure of murine C4b-binding protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                             83 CLRLCFFPFVENGHSESSGQTHLEGDTVQIICNTGYRLQNNENNISCVERGWSTPPKC
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SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
SIMILARITY: STRONG, TO FACTOR H.
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                                                                                                     Rodentia;
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                    T., Ogata R.T.,
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28, Last sequence update)
35, Last annotation update)
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37661 MW;
                                                                                                       Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
Sushi;
                      Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 434; DB 1;
pred. No. 2.23e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENT FACTOR H-LIKE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V -> L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_001982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId-VAR_001981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR_001980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8DC0D3F92A85E035 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> N (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                      L.P.,
                                                                                                                                                                                                                                                                                                       469
                        Reid K.B.M.,
                                                                                                                                                                                                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 330
      regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                        Tack B.F.;
                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
         component
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DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYL
                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
117 INDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSE 176
                                           170 SNPFPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLYGSPFIGCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the serum complement system.";
Blochemistry 26:4668-4674(1987).

-i- FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION: IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.

-i- SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M17122; AAA37312.1; ALT_INIT.
                                                                                                                                                                                                                   58 C-GPPP-AIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMVYCKPSGEWEISV-S 114
                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                      RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--W
                                                                                                                               --CAKKHCRNPGYLDNG-Y-VN-GETITFGSQIEFSCQEGFILVGSSTSSCEVRGKGVAW 169
                                                                                                                                                                        CKGPPPRENSEILSGSWSEQL-YSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO C4BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:88229; C4BP.
                                                                                                                                                                                                                                                                            118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127117; NBMSC4.
P10998; 1VVC.
                                                                                                                                                                                                                                                                                                h 12.9%;
Similarity 31.0%;
                                                                                                                                                                                                                                                                                                                                                                469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathway;
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                       Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                              WW.
                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                         Score 434; DB 1;
Pred. No. 2.23e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Repeat; Sushi; Signal.
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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MI
                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4B-BINDING PROTEIN.
6 X SUSHI (SCR) REPE
SUSHI 1.
                                                                                                                                                                                                                                                                                                                                                         41E137CB8D8C6321 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                     Mismatches 139;
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                                                                                                                                                                                                                                                                                                            Length 469;
                                                                                                                                                                                                                                                                Indels 41;
                                                                                                                                                                                                                                                                   Gaps
                                                                                          116
                                                                                                                                                                            59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γQ
                                                                                                                                                                           Matches
                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                      REPEAT
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08603; 1HFI.
PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skerka C., Timman C., Horstmann R.D., Zipfel P.E.; "Two additional human serum proteins structurally related to complement factor H. Evidence for a family of factor H-related to the complement factor H. Evidence for a family of factor H-related to the complement factor H. Evidence for a family of factor H-related to the complement factor H. Evidence for a family of factor H-related to the complement factor H-related to the complemen
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X64877; CAA46096.1; PIR; S24564; S24564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P36980;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59 PREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).

Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
307 CDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: EXTRACELLULAR.
-:- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
-:- SIMILARITY: STRONG, TO FACTOR H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92251200.
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                                                                     23 CDFPKINHGILYDEEKYKPFSQVPTGEVFYYSCEYNFVSPSKSFWTRITCAEEGWSPTPK 82
                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 148:3313-3318(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 SYMDYLRCTVNG-WEPEVP-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 KCTITGWI-PAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 VCTGSG-WNPQPSCEEMTC-LTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 VNKTVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECQGNGNWSSLPTCE-FDCDLPPAIVNGYYTS-MVYSKIT-LVTYECDKGYRLVGKAIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -N-GL--WSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CSFSKWKGTAPQCKA-LCQKPEVGNGTLS-DE-KDQY--VE-SENVTIQCDSGFAMLG-
                                                                                                                                                                           Similarity
50; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grycoprotern;
                                                                                                                                                                                                                                                                                                                         270 AA;
                                                                                                                                                                                                                                                                                                                                                                      119
119
119
128
128
128
1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
270
270
270
127
                                                                                                                                                                                                       12.8%;
                                                                                                                                                                                                                                                                                                                             30651 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sushi;
                                                                                                                                                                                                                                                                                                                                                                                           11; Signal.
POTENTIAL.
COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59.
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367
                                                                                                                                                          Score 431; DB 1;
Pred. No. 1.44e-82;
22; Mismatches 46
                                                                                                                                                                                                                                                                                                             POTENTIAL.
E1B2E9F139B217A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRECURSOR
                                                                                                                                                                   46;
                                                                                                                                                                                                                                Length 270;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-related
                                                                                                                                                          0;
                                                                                                                                                      Gaps
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S B

83 367

CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKC

140 424

CLRLCFFPFVENGHSESSGQTHLEGDTVQIICNTGYRLQNNENNISCVERGWSTPPKC

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Complement activation.";

J. Mol. Biol. 272:253-265(1997).

INTIBITING BOTH CLASSICAL AND ALTERNATIVE PATH ACTIVATION. BINDS C3B AND C4B.

SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE COMPLEMENT ACTIVATION (RCA).

COMPLEMENT ACTIVATION (RCA).

J. SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kotwal G.J., Moss B.;
"Analysis of a large cluster of nonessential genes
vaccinia virus terminal transposition mutant.";
Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kotwal G.J., Moss B.;
"Vaccinia virus encodes
to complement control p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                              antibody-dependent complement-enhanced and contributes to virulence.";
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-COPENHAGEN;
MEDLINE; 91021027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                         Wiles A.P., Shaw G.,
                                                                                                                                                                                                                                      Isaacs S.N., Kotwal G.J., Moss B.;
"Vaccinia virus complement-control protein prevents
                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                        FUNCTION.
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          This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                     MEDLINE;
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European
                                                                                                                                   studies of a viral protein
                                                                                                                                                                                                     Natl. Acad.
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ti E.;
gy 179:517-563(1990).
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stage; Poxviridae;
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P16109
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SIGNAL
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EMBL; M22812; AAA69605
EMBL; M35027; AAA47997
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                  Johnston G.I., Cook R.G., McEver "Cloning of GMP-140, a granule me endothelium: sequence similarity adhesion and inflammation."; Cell 56:1033-1044(1989).
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                                                                                                                 MEDLINE;
                                                                                                                                   SEQUENCE
                                                                                                                                                                          Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGD-GIYLKPVYKENERFQYKCKQGFVYKERGDAVCT-GSGWNPQ-PSC
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PF00084; sushi; 3D-structure.
                                                                       ; 89168432.
in G.I., Cook R.G
ig of GMP-140, a.c
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81; Conse
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Primates;
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03-DEC-97.
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AAA69605.1;
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35.2%;
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                                                                           McEver R.P.;
nule membrane
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4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 3.
SUSHI 4.
BY SIMILARITY.
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37; 1
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Pred. No. 3.54e-73;
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                                                                                                                                                                          Hominidae;
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                                                                                             R.P.;
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                                                        rane protein of platelets and proteins involved in cell
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PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS0118; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS00615; C_TYPE_LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PFAM; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
"The P-selectin gene is highly polymorphic: reduced frequency of the
Pro715 allele carriers in patients with myocardial infarction.";
Hum. Mol. Genet. 7:1277-1284(1998)
-1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LICAND RECCONIZED IS SIAVIL-LEWIS X.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANG PROTEIN.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANG PROTEIN.
-1- SISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL.
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-STRUCTURE MODELING OF MEDLINE; 94093388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure and function of the epidermal growth factor domain of P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE CELL SURFACE.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.

DATABASE: NAME-PROW; NOTE-CD guide CD62P entry;
                                                                                                                                                                                                                                                                                                                                                 ; M60232; AAA35910.1;
; M60233; AAA35910.1;
; M25322; -; NOT_ANNOT
A30359; A30359.
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                                                                                                                                                                                                                                                         173610;
   PF00059;
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M60217; AAA35910.1;
M60218; AAA35910.1;
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97057176.
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AAA35910.1;
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lectin_c; 1.
sushi; 9.
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24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTP-FGSFR-L 80
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal;
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                                Conservative
                                                                AA;
                                       11.6%;
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                                                                MW;
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                              Score 390; DB 1;
Pred. No. 1.41e-71;
87; Mismatches 191
                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                       T -> P (REDUCED FREQUENCY IN PATIENTS WITH MYOCARDIAL INFARCTION).
/FTId=VAR_004195.
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C-TYPE LECTIN (SHORT FORM)
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EXTRACELLULAR (POTENTIAL).
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at; Polymorphism; 3D-structure.
                                                               FBC407BA2579F6EB CRC64;
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                                             Length 830;
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED BETA-2-GLYCOPROTEIN) (APC INHIBITOR) (B2GPI).
                                          APOH_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                           "Characterization, expression and evolution of mouse beta glycoprotein I (apolipoprotein H)."; Biochem. Biophys. Res. Commun. 200:1521-1528(1994).
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"Molecular cloning of mouse beta
gene to chromosome 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Mus musculus (Mouse).
Thiramvota; Metazoa; Chordata; Craniata; Vertebrata;
Murinae; Murinae;
                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                        Whitehead A.S.;
                                                                                                                                                                                                                                                                                                                        MEDLINE;
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mouse beta 2-glycoprotein I
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EMBL; S70439;
EMBL; Y11356;
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        LEM3_RAT STANDARD; PRT; 768 AA.
p98106;
01-FEB-1996 (Rel. 33, Created)
11-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
p-SELECTIN PRECURSOR (GRAULLE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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 SELP.
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                                                                                                                                258 I-YTPHRIK 265
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                                                                                                                                                       VLYQGMRVK 281
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                                                                                                                                                                                                                              SGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLMSNEKPQCVEISC-LPPRVEN
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                                                                                                                                                                                GDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTGSG-WNPQPSCEEMTCLTPYIPNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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PROSITE; PS01022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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Gene 145:251-255(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                             Eutheria; Primates;
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                                                    Chordata; Craniata; Vertebrata; Mammalia;
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P02749;
21-JUL-1986 (Rel. 01, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
BETA-2-GIXCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
APOH OR B2G1.
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Homo

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Day J.K., Arnaud P.;
Werner P., Arnaud P.;
"Molecular cloning and sequence analysis of the apolipoprotein H (beta 2-glycoprotein I).";
apolipoprotein Lab. Res. 21:256-263(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence and apolipoprotein H (beta 2-Gene 108:293-298(1991).
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                                                                                                               "Qualitative analysis of the car
apolipoprotein H.";
J. Protein Cho-
                                                                                                                                                                                                                                                     Steinkkasserer A., Campbell I.D., Sim
                                                                                                                                                                                                                                                                                                                          Lozier J., Takahashi N., Putnam F.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Kristensen T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular definition of human beta 2-glyco
CDNA cloning and inter-species differences
alternation of anticardiolipin binding.";
Int. Immunol. 3:1217-1221(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasuda T., Koike T.:
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                                                                                                                                                                                                            Steinkkasserer A., Barlow P.N., Willis A.C., Kertesz Z., Campbell I.D., Sim R.B., Norman D.G.; "Activity, disulphide mapping and structural modelling of the fifth domain of human beta 2-glycoprotein I."; FBS Lett. 313:193-197(1992).
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Bouma B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G., Schouten A., Simmelink M.J.A., Derksen R.H.W.M., Kroon J., Gros P., "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids based on its crystal structure.";
                                                       MEDLINE; 99437994
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J.R., O'Hara P.J.,
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                                                                                      ANGSTROMS)
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Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.; "Human beta 2-glycoprotein I: molecular analysis of DNA and amino acid polymorphism.";
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Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;

Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;

"Identification of structural mutations in the fifth domain of appolipoprotein H (beta-2-glycoprotein I) which affect phospholi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MA ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE B TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
TISSUE SPECIFICITY: PLASMA.
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                              C; X58100; CAA41113.1;

C; X53895; CAA37664.1;

CX57847; CAA40976.1;

CAA40977;

M62839; AAA51766.1;

CY11493; CAA72279.1;

CY11494; CAA72279.1; JOIN

CAA72279.1; JOIN
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FUNCTION: BINDS TO VARIOUS KINDS
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                                                                                                             154 RVYKPSAG-NNSLYRDTAV-FECLPQHAMFGNDTITCTTHGNWTKL-PECREVKCPFPSR 210
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                                                                                                    T--T-FEYPNTISFSCNTGFYLNGA-DSAKCTEEGKWSPELPVCAPIICDPPSIPTFATL 153
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/FIId-vAR_008170.
W -> S (IN APOH*3W; LOSS OF PHOSPHATIDYLSERINE-BINDING).
/FIId=VAR_008171.
S -> C (IN REF. 7).
C -> N (IN REF. 7).
C -> N (IN REF. 7).
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Pred. No. 1.79e-65;
54; Mismatches 106; Indels 21;
                                                                                                                                                                                                                                                                                                                   S -> N (IN APOH*1).

/FTIG=VAR_008169.

V -> L (IN 23% OF THE POPULATION).

/FTId=VAR_000673.

C -> G (LOSS OF PHOSPHATIDYLSERINE-
                                                                                                                                                                                                                                                                                                              BINDING)
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                                                                                                                                                                                                            Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:51:06 2000; MasPar time 36.70 Seconds 808.665 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-09-316-163-14 (1-428) from US09316163.pep 3371 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428

Scoring table: PAM 150 Gap 11

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

225878 seqs, 69334122 residues

Database:

sptrembl12
1:sp_darchea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_darchea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 45.569; Variance 69.358; scale 0.657

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 22 3 3 3 4 4 4 4 4 7 7 8 8 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOAMES C.J., DAY A.J., SIM R.B.; "Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b."; Biochem. J. 315:523-531(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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136 NGRIVSGAAEDDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPP 195
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                                                                  63 NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
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                                                                                                                                                                                                                                                                                                                                                                                                   y Match 51.0%;
Local Similarity 58.4%;
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                                                                                                                                                                           GSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWINDIPICEVVKCLPVTELE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSPAVPCLRKCYFPYLENGYNQNYGRKFVQGKSIDVACHPGYALPKAQTTVTCMENGWSP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWDHIHCTQDG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPRCIRV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00084; sushi; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669
669 AA;
                                                                                                                                                                                                                                                                                                                                                                Conservative
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75683 MW; FAF0D174 CRC32;
                                                                                                                                                                                                                                                                                                                                                  Score 1720; DB 6; I
Pred. No. 0.00e+00;
64; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 669;
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                                Q61405 PRELIMINARY; PRT; 303 AA.
Q61405;
Q61405;
Q61-NOV-1996 (TrEMBLrel. 01, Created)
Q61-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q61-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q61407 PRELIMINARY; PRT; 452 AA.
Q61407;
Q61407;
Q1-NOV-1996 (TremBirel. 01, Created)
Q1-NOV-1996 (TremBirel. 12, Last sequence update)
Q1-NOV-1999 (TremBirel. 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIK D.P., MUNOZ-CANOVES P., CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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VIK D.P., MUNOZ-CANOVES P.,
                                                                                                                                                                                                                                                                                                                                                      415
                                                                                                                                                                                                                                                                                                                                                                                                          194 ENGWSPPPKCIRIK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSY-WDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 RLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCIFHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYRCDNGFSPPS-GYSWDYL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 RLYY--SYRGYFFARVNQQFVYSCDHHFVPPSQRSWDHLACTAEGWSPEEPCLRQCIFNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                      ENGWSPPPKCVRIK 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCTAQGWEPEVPCVRKCVFHYVENGDSAYWEKIYVQGQSLKVQCYNGYSLQNGQDIMTCT 193
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Similarity 71.1%;
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452 AA; 51602 MW; 45C0BF61 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1136; DB 11;
Pred. No. 3.25e-267;
22; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOZONO H., MARTIN L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOZONO H., MARTIN L.G.,
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                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q61408;
Q61408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 265:3193-3201(1990).
EMBL; M29007; AAA37413.1; -.
HSSP; P10998; IVVC.
PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification and sequence analysis of four complement factor H-
related transcripts in mouse liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAPLIN D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 90153969.
VIK D.P., MUNOZ-CANOVES P., KOZONO H., MARTIN L.G., TACK B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                      "Identification and sequence analysis of four complement factor related transcripts in mouse liver.";
J. Biol. Chem. 265:3193-3201(1990).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 90153969.
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                 CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                VIK D.P., MUNOZ-CANOVES P., KOZONO H., MARTIN L.G., TACK B.F.,
                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 WIPVPRCTLKPCEFPOFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPS-GYSWDYL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
 413
                           134
                                                      353
                                                                                                            293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                          14 LTAMLSTAKGEVKSCEFPQFKYGRLYFEEILRPNFPVSIGNKYSYKCDNGFSPPSGLFWD 73
                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RCTAQGWEPEVPCVRKCVFHYVENGDSTYWEKIYVQGQSLKVQCYNGYSLQNGQDTMTCT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGWSPPPKCIRIN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCT
                 CTENGWSPPPKCIRIK 149
                                                     YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYY 412
                                                                                YLRCTVQGWKPEVPCVRKCVFHYVENGEFAYWEKIYVQGQSLKVQCYNGYSLQNGQDTMT 133
 CTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.5%;
il Similarity 70.6%;
137; Conservative
                                                                                                                                                                                                            PF00084; sushi; 13.
PF00084; sushi; 13.
                                                                                                                                                                                                                                               M29009; AAA37416.1; P08603; 1HCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                Similarity
90; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                     Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 AA;
                                                                                                                                                                23.4%;
llarity 66.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata;
                                                                                                                                                              Score 790; DB 11;
Pred. No. 4.80e-173;
24; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.70e 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39350FD1 CRC32;
                                                                                                                                                                                                                        23644778 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.70e-265;
atches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                           Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 303;
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                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
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RR ROCC OCC DIT
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Best Local
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Q91275

Q91275;

Q1 NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
Paralabrax nebulifer (barred sand bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii.
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Percoidei; Serranidae; Paralabrax.
                                                                                                                                                                                 O08569 PRELIMINARY; PRT; 533 AA.

008569; O1-JUL-1997 (TrEMBLrel. 04, Created)

01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

ACROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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HSSP; P08603; 1HFH.
PFAM; PF00084; sushi; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAHMEN A., KAIDOH T., ZIPFEL P.F., GIGLI I.; "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94318039.
                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
STRAIN-HARTLEY; TISSUE-TESTIS.
                                SEQUENCE FROM N.A.
                                                                                            Eutheria; Rodentia; Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 NDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQVIGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AEPDQEYYFGQVVRFECNSGFKI-EGQKEMHCSENGLWSNEKPQCVEISCLPPRVENGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 HYVEYGESSYWQRR-YIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 YPGGRQVRVGCNVGY-S-GFFKLVCVEGKW-ETRGAK-CQPRSCGHPGDAQFADFHLAEG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENIQDAVIVGTDKQIYNLNQKAIYACGEG-N--RGRITLTCGENGWSGDRKCT-VK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWINDIPICEVVKCLPVTELENGRIVSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDSWDVRSWERY---TLDDNTRYWCKRGYKRTGGVTWA--TCGRNGWMPNPLCEVKTCSK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP-HRIKHRIDDEIRYEC-KNGFYPATR-SPV-SKCTITG-WIPAPRCSLKPCDFPQFKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGAIREYKENDVLHYECDRAFKHIDRPSTCIKQGIKAEWSPTPLCESIKCRLTIMDGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PEEAT-FGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIENGNV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYLKPVYKENERFQYKCKQGFVYKERGDA-VCTG--SGWNPQPSCEEMTCLTPYIPNGIY
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Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1053 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 683; DB 13; Pred. No. 2.44e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1053;
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                                                                                                                                                                                                                     Q28769;
01-NOV-1996 (TIEMBLIET 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
COMPLEMENT RECEPTOR (FRAGMENT).
                                                                              TISSUE-BONE MARROW;
BIRMINGHAM D.J., LOGAR C.M., SHEN X.P., CHEN W
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
                                                 EMBL; L77977; AAA99004.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                          Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
      SEQUENÇE
                                  PFAM; PF00084; sushi; 7.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                  Papio.
                                                                                                                                                                            Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                Q28769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97284752.
FRIDAY B.B., MAULIT M.T., BLOBEL C., WINFREY V.P., CLSON G.E., KIM K.S., GERTON G.L.;
"AM67, a secretory component of the guinea pig sperm acrosomal matrix, is related to mouse sperm protein sp56 and the complement component 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 272:12714-12722(1997).
EMBL: U75654, AAC13888.1; -.
HSSP: P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                        394 AKVQCHSGYSLPNGQDTYYCTEN-GWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                         434 VTIHCDSGYEVVGPQNII-CSENRTWTPEIPKC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 DC-GPPPILPFASPVIQSY-ETNFRTGTALKYNCHRGYWRVNSSHVICDINGSWI-YN-V 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 15.4%; Score 520; DB 11; Length 533; Local Similarity 27.2%; Pred. No. 3.02e-101; es 123; Conservative 105; Mismatches 179; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YMCDEGYYPISADGRS--SCQADGMWNPKMPACESAVCLKPDILNGKLSVEKDHYTETEN 433
                                                                                                                                                                                                                                                                                                                                                                                                                                      Y-CDNGFTTPSQSYWDYLRCTVNG-WEPEVP-CLRQ-CIFHYVEYGESSYWQRRYIEGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATRSPVS-KCTIT-GWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPI-G-KEYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPNEPRTVTCQENLKWAISKGCERVCCPTPNMEKMRII-NE-RRDFTGVCVYAYEDYIF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVC-TGSGWNPQ-PSCEEMTC--LT--PYIP-N-GIYT-PHRIKHRIDDEIRYECKNGFY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHCEANSKWYPSIPTCEPNGCIDLPEVPYISWERNVLSLKNQEIFEIGSLLKYDCKTGYR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VANKTYGVWSSNPPTCEKVICROPHIPKGIFLSGFGFYYTYKDTLVISCKKGYILRGSSI 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADG---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SEN--GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCK-NGEWVPSNPS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FCAKKRCRNPGELANG--KVEIITDLLFGSTIEFSCSKGYSLIGSTT-SQCESQGKTVD 140
 52,2,AA;
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 AA;
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29
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     56626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACROSOMAL MATRIX COMPONENT AM67 60EEA526 CRC32;
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7862072C CRC32;
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                                                             N W.;
лВЛ databases.
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                                                                                                                                                                                                                                                               DOHI N., SAKURADA C., NONAKA M., OKADA N., OKADA H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; L36532; AAA91821.1; -.
EMBL; D42115; BAA22548.1; -.
HSSP; P10998; 1VVC.
PFAM; PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 96006570.
QUIGG R.J., LO C.F., ALEXANDER J.J., SNEED A.E., MOXLEY G. III;
"Molecular characterization of rat Crry: widespread distribution of
two alternative forms of Crry mrna.";
Timmunogenetics 42:362-367(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      063135;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
COMPLEMENT REGULATORY PROTEIN.
                                                                                                                                                                                                                                                         SEQUENCE
151 AEAPICESIPCEIPPSIPNGDFFS--PNRE-DFHYGMVVTYQCNTDARGKKLFNLVGEPS
                                                                                                                                                                                                                                                                                                                                                                              TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q63135
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                         37 QCPAPPLFPYAKPINPT-DESTFPVGTSLKYECRPGYIKRQFSIT-CEVNSVWT-S-PQD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 PICTVKSCDDFLGQLPHGRVLF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 CEEMTCLTP-YIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIP-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 CSRV-COPPEILHGEHTPSHQDFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWNPEA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 VEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 IIPNKCMPPNVENGVLVSVNRSLFSLNEVVEFRCQPGFVMKGPRHVQCQALNKWEPELPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 FPVGTYLKYECLPGYHG-KPFSIICLKNSVWTSAK-DK-CTRKSCRNPKD-PVNGM-VHV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.2%;
Local Similarity 33.2%;
es 107; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                   | CRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEID--YRECDAD-GWT 117
                                                                    VCIRKQCETPLDPQNG-I-VHVNTDIRFGSSITYTCNEGYRLIGSSSAMCIISDQSVAWD 150
                                                                                                         DCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCK-NGEWVPSNPSR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVSGAAEPDQEYY-FGQVVRFECN--SGFK-I-E--GQKEMHC-S-EN--GLWSNEKPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIS-TS---REYFPYGSVVTYRCNLGSGRKKLFELVGEPSIYCTSKDDQVGIWSGPAPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKDIQFGSQINYSCNKGYRLIGSSSATCIISGNTVIWDNETPICEIIPCGLPPT-IANGD
                                                                                                                                                                                                    14.0%;
Similarity 26.9%;
                                                                                                                                                                                                                                                      559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                               Conservative 114; Mismatches 170;
                                                                                                                                                                                                                                                      61680 MW; C87EEC58 CRC32;
                                                                                                                                                                                                Score 471; DB 11;
Pred. No. 1.66e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 480; DB 6; Length 522;
Pred. No. 7.77e-91;
74; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559
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                                                                                                                                                                                                                 Length 559;
                                                                                                                                                                              Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
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014006;
01-NOV-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B., HARRIS T.J., SIM R "Sequence analysis of a CDNA clone encoding the C-terminal end human complement factor H.";

Biosci. Rep. 7:201-207(1987).

EMBL; M17517: AAA52016.1; -.

HSSE; P08603; 1HFH.

HFAM; PF00084; sushi; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hur.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENT
            486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                     261
                                                                                                                             428
                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                              143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 EGQSAKVQCHSGYSLPNGQDTYYCTENGWSPP-PKCV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280
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VSRQMSKYP-S-GERVRYQCRSPYEMFGDE--EVM-CLNGNWTEPPQCKDSTGKCGPPPP
                                                                                                                                                                             GIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLT-PYIPNGIYT
                                                                                                                                                                                                                                  VAHMSDSYQYGEEVTYKCFEGFGIDGPAIAKCLGEKWSHPPSCIKTDCLSLPSFENAIPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNYRDGEKVSVLCQENY-LIQEGEEITCKDGRW-QSIPLCVEKIPCSQPPQIEHGTINSS 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG
                                                           PHRIK-HRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHGRLYY 319
                                                                                                                 GEKKDVYKAGEQVTYTC-ATYYKMDGASNVTCINSRWTGRPTCRDTSCVNPPTVQNA-YI
                                                                                                                                                                                                                                                                                                 AAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCL-PPRVENGD
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                                                                                                                                                                                                                                                                                                                                                          RS-SQESYAHGTKLSYTCEGGFRISEENETTCY-MGKWSSP-PQCEGLPCKSPPEISHGV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VALECEDGYTLEGSSQSQC-QSDAS-WDPPLPKCVSQVICKLPQDMSGFQKGLQMKKDYY 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGDNVALECEDGYTLEGSSQSQCQSDASWDPPLPKCV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVP-CLRQ--CIFHYVEYG-ESSYWQRR-YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYPATRSPVSKCTITG----WIPA-PRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KERGDAVCTG-SGWNPQ-PSC-EEMTC--LTPYIPNG-IYTPHRIKHRIDDEIRYECKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGDSSVYCRSLNRWEPQLPSCFKVKSCGAFLGELPNGHVFVPQNL-Q-LGAKVTFVCNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC-S-EN--GLWSNEKPQCVEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YQLKGNSSSHCVLDGVESIWNSSVPVCEQVICKLPQDMSGFQKGLQMKKDYY---YGDN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 13.9%;
Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TIEMBLrel. 01, Created)
(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 12, Last annotation update)
H FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 470; DB 4;
Pred. No. 3.02e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F4AB5238 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 201; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Mammalia; ae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 657;
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Best Local
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NON_TER
SEQUENCE
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KURTZ C.B., O'TOOLE E., CHRISTENSEN S.M., WEIS J.H.;

KURTZ C.B., O'TOOLE E., CHRISTENSEN S.M., WEIS J.H.;

"The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1.";

j. Immunol. 144:3581-3591(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cofactor protein.";
J. Exp. Med. 181:151-159(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse complement regulatory protein Crry/p65 uses the mechanisms of both human decay-accelerating factor and \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 21-367 FROM N.A. MEDLINE; 95105691.
KIM Y.U., KINOSHITA T., MOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99254
Q99254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement pathway; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING OF CR2 GENE TRANSCRIPTS PREDICTS TWO DISTINCT GENE PRODUCTS THAT SHARE HOMOLOGOUS DOMAINS WITH BOTH HUMAN CR2 AND CR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                      157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: B LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOLERS V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALTERNATIVELY SPLICED VERSION) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320
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                                                                                           83
                                                                                                                                                                                               24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                  42 FAIGTTWEYKCRPGYFRKSFIIT-CLETSKW--SDAQQFCKRKPCMNPQEPLHGSVHINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L; U17128; AAA78271.1; -.
L; U17123; AAA78271.1; JOINED.
L; U17124; AAA78271.1; JOINED.
L; U17125; AAA78271.1; JOINED.
L; U17126; AAA78271.1; JOINED.
L; U17127; AAA78271.1; JOINED.
L; U17127; AAA78271.1; JOINED.
GSEFEFGAKVVYTCDEGYQLLGE--IDYRECDADG-WTNDIPICEVVKCLPVTELENGRI
                                                                                                                                       G--IEFGSTITYSCNQGYRLIGDSSATCIVSDNTVMWDNDMPLCESIPCESPPAISNGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:88489; Cr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGW-EP-EV-PCLRQC-IFHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U17127; AAA78271.1; M36470; AAA37449.1; P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00084; sushi; 10.
                                                                                                                                                                                                                                                                                                                                             h 13.9%;
Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                             679
679 AA;
                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             679
74916 MW;
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                                                                                                                                                                                                                                                                                                                                             Score 470; DB 11;
Pred. No. 3.02e-88;
                                                                                                                                                                                                                                                                                                                72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENT RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                BF08AC75
                                                                                                                                                                                                                                                                                                                Mismatches 111;
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                                                                                                                                                                                                                                                                                                                                                                  Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat;
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                                                                                                                                                                                                                                                                                                             35;
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RESULT
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Best Local Similarity 31.8%;
Matches 118; Conservative
Q92496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O29528 PRELIMINARY; PRT; 1911 AA.
029528; PRELIMINARY; PRT; 1911 AA.
029528; Created)
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases EMBL; L39791; AAA62170.1; -. HSSP; P08603; IHCC. HSSP; P08603; LHCC. PFAM; PF00084; sushi; 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLEMENZA L., SUBRAMANIAN B.V., NICKELLS M.W., ATKINSON J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                1193 RSLWNNSVPVC 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 VSGAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHC-S-EN--GLWSNEKPQCVE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 VEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850 FPIGTSLKYECRPEYYG-KPFSITCLD-NLVWSSPKDVCKRKSCKTPPD-PVNGM-VHVI 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ISCLPPRVENG--DGIYLKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVKCPMPEIENGLVESGF-KHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPPLPTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVSGAAEPDQEYY-FGQVVRFECN--SGFK-I-E--GQKEMHC-S-EN--GLWSNEKPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEFEFGAKVYYTCDEGYQLLGEIDYREC--DAD-G-WINDIPICEVYKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDIQVGSRINYSCTTGHRLIGHSS-AECIISGNTAHWSTKPPICQRIPCGLP-PPIANGD 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG
                                                                                                                                                                    NG-WEPEVP-C
                                                                                                                                                                                                                                                                                                                            APRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTV 358
                                                                                                                                                                                                                                                                                                                                                                                                    APRCAVKSCD--DF-LGQLHHGRVLVP-FNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGM 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEEMTCLTP-YIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSRV-CQPPPEILHGEHTPSHQDKFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWSPE 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIPNKCMPPNVENGILVSVNRSLFSLNEVVEFRCQPGFVMKGPRRVQCQALNKWEPELPS 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIS--T--NREYFHYGSVVTYRCNLGSGRKKLFELVGEPSIYCTSKDDQVGIWSGPAPQC 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1911 19
1911 AA;
        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 456; DB 6; Length 1911;
Pred. No. 1.25e-84;
81; Mismatches 128; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 128; Indels 44;
                        331
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01-FEB-1997 (TIEMBLrel. 02, Created)
01-FEB-1997 (TIEMBLrel. 02, Last sequence update)
01-NOV-1999 (TIEMBLREL. 12, Last annotation updat
COMPLEMENT FACTOR H-RELATED PROTEIN 4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                       VIK D.P., MUNOZ-CANOVES P., KOZONO H., MARTIN L.G., TACK B.F., CHAPLIN D.D.;
"Identification and sequence analysis of four complement factor related transcripts in mouse liver.";
related transcripts in mouse liver.";
Biol. Chem. 265:3193-3201(1990).
EMBL; M29008; AAA37414.1; -.
HSSP; P08603; 1HFI.
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"The human factor H-related protein 4 (FHR-4). A novel short consensus repeat-containing protein is associated with human triglyceride-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).

Homo sapiens (Human).

Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                   FRAM; PF00084; sushi; 4.

SECULENCE 343 AA; 38443 MW; 6CED5090 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 90153969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X98337; CAA66980.1; HSSP; P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoproteins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 SGSITCLQNGWSAQPICIKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 DYLRCTVNGWEPEVPCLRQCI-FHY-VEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 ITGWIPAPRC-SLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYW 351
293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
                                                                                                                                            Local Similarity 41.4%; hes 55; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 13.3%;
Local Similarity 43.6%;
hes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 DYIHCTQDGWLPTVPCLRTCSKSDIEIENGFISESSSIYILNKEIQYKCKPGYATADGNS 128
                                                                                 14 LTSWFSTAKGEVSLCDFPKIRHGILYDEKKNEPFSSVLSGKILYYSCEYNFASPSNSFWT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LTLWVSCANGQEVKPCDFPEIQHGGLYYKSLRRLYFPAAAGQSYSYYCDQNFVTPSGSYW 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00084; sushi; 5.
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331 AA;
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37325 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                              Score 447; DB 11;
Pred. No. 2.60e-82;
29; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 448; DB 4;
Pred. No. 1.44e-82;
22; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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COMPLEMENT FACTOR H-RELATED PROTEIN 4.

2505D66C CRC32;
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                                                                                                                                                                                                                                                        Length 343;
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Best Local Similarity 32.3%;
Matches 104; Conservative
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SEQUENCE
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029531; O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 94292799.

BIRMINGHAM D.J., SHEN X.P., HOURCADE D., NICKELLS M.W., ATKINSON J.P.;

"Primary sequence of an alternatively spliced form of CR1. Candidate
for the 75,000 M(r) complement receptor expressed on chimpanzee
for the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L24921; AAA51439.1; -. HSSP; P10998; IVVC. PFAM; PF00084; sushi; 9.
                                                                                                                                                                                                                                                                                                                                                               189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCOPGFVMKGPPRVKCOALNKWEPELPSC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:||| |||:
413 CTENGWSPPPKCV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
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                                                                                                                                                                               EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 188 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 | 189 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                       PTCEVKSCDDFMGQLLNGRVLF 347
                                                                                                                                                                                                                                                                       SRV-COPPPDVLHAERTORDKDNFSPGQEVFYSCEPG-Y-DLRGAASLRCTPQGDWSPAT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAEEGWSITPKCI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 POTENTIAL.
>661 COMPLEMENT RECEPTO
661
1, 72966 MW; 9D78E262 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 449; DB 6; Length 661; Pred. No. 7.94e-83; 73; Mismatches 107; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
COMPLEMENT RECEPTOR 1.
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                                                                                                                                                                               299
                                                                                                                                                                                                                                                                                                                                                               244
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